

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
1 April 2004 (01.04.2004)

PCT

(10) International Publication Number  
WO 2004/026888 A2

(51) International Patent Classification<sup>7</sup>: C07H

(21) International Application Number:  
PCT/US2003/029577

(22) International Filing Date:  
19 September 2003 (19.09.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/412,479 19 September 2002 (19.09.2002) US

(71) Applicants (for all designated States except US): COLEY PHARMACEUTICAL GMBH [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). UNIVERSITY OF SASKATCHEWAN [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). QIAGEN GMBH [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).

(72) Inventors; and

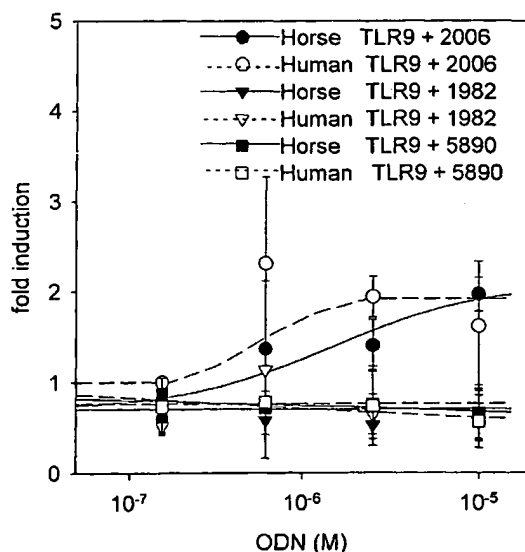
(75) Inventors/Applicants (for US only): LIPFORD, Grayson, B. [US/US]; 38 Bates Road, Watertown, MA 02472 (US). MOOKHERJEE, Neeloffer [IN/CA]; Apt 408, 2233 Allison Road,, Vancouver, BC V6T 1T7 (CA). BABIUK, Lorne [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). BROWNLIE, Robert [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). GRIEBEL, Philip [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). MUTWIRI, George [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). HECKER, Rolf [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).

(74) Agent: STEELE, Alan, W.; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).

(81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU; CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.

WO 2004/026888 A2



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

## TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

### Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory  
5 CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune  
system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001)  
*Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for  
biological activity and it is reported that optimal CpG DNA sequences can vary among  
species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

10 Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN.  
Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9  
recognizes CpG DNA is not understood.

### Summary of the Invention

15 Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal  
in response to CpG DNA. To date, the amino acid sequences only of human and murine  
TLR9 have been reported, and, interestingly, these two species are known to prefer different  
CpG motifs. The structural basis for this species-specific CpG motif preference has not yet  
been fully elucidated. The instant invention provides, in part, novel amino acid and  
20 nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are  
useful for elucidating certain key structural features of TLR9. Specifically, comparison of  
sequences of murine, human, and these novel TLR9 sequences permits identification of areas  
of highly conserved sequence, areas of group conservation, and areas of hypervariability. In  
addition, such comparisons permit an assessment of evolutionary relatedness among TLR9  
25 molecules of the various species, as well as an assessment of inter-species homologies.  
Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9  
that may be involved in the CpG binding site, as well as amino acids involved in conferring  
species specificity for particular CpG motifs. Such information may be used to design and  
construct novel TLR9 molecules which incorporate specific point or regional mutations and  
30 which possess desired ligand binding characteristics. Such information may also be useful in  
designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an  
5 extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand,  
15 such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID  
20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid  
25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the  
30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided  
5 by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to  
10 one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments  
15 the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species. The method involves aligning protein sequences of TLR9 of a first species,  
20 TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is  
25 identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b)  
30 differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment  
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide  
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in  
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),  
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and  
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes  
 5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one  
 embodiment the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B. In one  
 embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or  
 CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test  
 10 compounds. In one embodiment the response mediated by the TLR9 signal transduction  
 pathway is measured quantitatively and the response mediated by the TLR9 signal  
 transduction pathway associated with each of the plurality of test compounds is compared  
 with a response arising as a result of an interaction between the functional TLR9 and a  
 reference immunostimulatory compound.

#### 15 Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid  
 sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig  
 (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid  
 20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9  
 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and  
 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six  
 sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and  
 human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,  
 porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected  
 oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

#### 30 Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9  
 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key  
 features of the primary sequences of these and related TLR molecules, including previously



- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as

10 used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as

15 to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from

20 the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See

25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on

30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

- 9 -

## SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI  
 HHLHNLDVHLPNVRQLNLKWNCPPPGLSPLHFSCRTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
 5 SHTNIVLDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTDAFLGLSNLTHLSLKYNNTLEVPRQLPPSLEYL  
 LLSYNLIVKLGAEDLANLTSRLMDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSLHSLN  
 SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDSLNFYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
 FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVPW  
 PASLTPALPSTPVSKNFMVRCKNLRTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
 10 VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
 VEYLDGSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNLYPKSLTKLSFRDNHLSFFNWSSLA  
 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVLDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL  
 AVAVGTVLPPLLQHLGWDVWYCFHLCLAWLPPLTRGRRSAQALPYDAFVVDKAQSAVADWVYNELRVRLERERG  
 15 RRALRLCLEDRDLPGQTLFENLWASIYGRKTLFVLAHTDKVSGLLRTSFLLAQQRLLDRKDVVVLVILRPDA  
 HRSRYVRLRQLRCRQSVLFWPHQPNGQGSFWAQLSTALTRDNHHFYNRNFCRGPTAE

## SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI  
 20 HHLHNLDVHLPNVRQLNLKWNCPPPGLSPLHFSCRTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
 SHTNIVLDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTDAFLGLSNLTHLSLKYNNTLEVPRQLPPSLEYL  
 LLSYNLIVKLGAEDLANLTSRLMDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSLHSLN  
 SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDSLNFYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
 FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVPW  
 25 PASLTPALPSTPVSKNFMVRCKNLRTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
 VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
 VEYLDGSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNLYPKSLTKLSFRDNHLSFFNWSSLA  
 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVLDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG  
 30

## SEQ ID NO:3 (Rat TLR9)

atgggtctctgctgcaggaacctgcaccccttgctctctcctggtagcagccgcagtgctggctgaggtctggcc  
 ctgggtacctgcctgccttccctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg  
 aagctgtgctcctcactctctgctgcgcagaaccccggtccaacatcaccagccttctccttgatcgccaaccgcac  
 35 caccacctgcacaacctcgactttgtccacctgccaacgtgcgacagctgaacctcaagtggaaactgtccgccc  
 cctggcctcagcccttgcaacttctcctgcccgcagcattgagcccaaaccttctcctggctatgcgcagctg  
 gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgccagctccctgacgaatctgagccta  
 agccacaccaacatcctggtagctgacccagcagcctcgctggcctgcacagcctgcgagttctctcatggac  
 gggaaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgacgccttctcctgggcttgagcaac  
 40 ctccaccttgctcccttaagtataacaacctcacagaggtgcccccgcaactgcccccgagcctggagtacctc  
 ctgctgtcctataacctcatcgctcaagctggggcggaagacctagccaacctgacctcccttcgaatgcttgat  
 gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgccggcgagaagtcctcttgatctg  
 caccctcagactttccatcacctgagccacctgaaggcctgggtgctgaaggacagttctctccactcgctgaac  
 tccaagtgggtccaagggtctggcgaaacctctcggtgctggacctaaagcgagaacttctctacgagagcatcaac  
 45 aaaaccagcgcccttcagaacctgacctgctgcgcaagctcgacctgtccttcaattactgcaagaaggatcg  
 ttcgccccctccacctggcaagtctcttcaagagcctgggtgctgctgagcagctgaacatgaacggcatctt  
 ttccgcttactcaacaagaacacgctcaggtggctgggtgctgccccagctccacacgctccacttcaaatg  
 aattcatcaaccagcgagctccttagtacctccgagcccttcgcttctgtggacctgtccaataat  
 cgcacagcgggcctccaacgctgtccagagtcgccccgaaaaggcagacgagggcgagaaggggggttccatgg  
 50 cctgcaagtctcaccctcagctctcccgagcactccgctctcaagaacttcatgggtcaggtgtaagaacctcaga  
 ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctcccatctccag  
 tgtctgagcctgagccacaactgcacgaggtgtcaatggctctcagttcctgcccgtgaccaacctgaag  
 gtgctggacctgtcctataacaagctggacctgtacattcgaaatcggttcagtgagctcccacagttgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggatagggcacaacttcagttttctggccaatctg  
tccaggttacagaaccttagcctggcacacaaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcattgtgggacgaggaggacctttacctctattttctc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaaacctcaac  
5 tacctccccaaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctctggcc  
ttcctgccccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcacccctgccta  
ggcagctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttctttgtctctggcg  
gtagagctaaaagggtcaacctcagccataaacatcctcaagactgtggatcgctcctgggttgggccccattgtg  
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcacctttgtgagacttactg  
10 ctggaagtgcagaccaaggtgcctggcctggctaacgggtgtgaagtgtggcagctccccgccagctgcaggggccgc  
agcatctttgcgcaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggcctttactcctg  
gctgtggcctgtggcgacgggtgtgcctttactgcagcatctctgcggctgggacgtctggtagctgttccatctg  
tgcttgccatggctacctttgctgacctgtggcggcgacgcgccccagctctccttatgatgccttcgtgggtg  
ttcgataaggcgacagagcgcggttgctgactgggtgtataacgagcttcgagtgcggttagaggagcgggcggtg  
15 cgccgagcctacgcttgggtctggaggacgagattggctgcctggccagacactcttcgagaacctctggggcc  
tccatctatggcagccgcaagactctgtttgtgctggccacacggacaaggtcagtgccctctcgccgaccagc  
ttcctgctggctcagcagcgctgtggaggacgcaaggacgtgggtgttgggtgatcctgcgccccgatgcc  
caccgctcccgctacgtgcgactgcgccagcgctctgcgccagagtgctcttctggccccatcagcccaac  
gggcagggcagctctggggccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc  
20 tgccgggggacctacagcagaatag

## SEQ ID NO:4 (Rat TLR9)

atgggttctctgtcgcaggacctgcaccccttgtctctcctgggtacaggccgcagtgctggctgaggtctctggcc  
ctgggtacctgctgcttcttacctgtgaacctgaagcctcatggcctggtagactgcaactggctcttctctg  
25 aagctgtgctcacttctctgcgcgacacccgttccaacatcaccagccttctctgactgcgaacccgcac  
caccacctgcacaacctcgactttgtccacctgcccacgtgcgacagctgaacctcaagtggaactgtccgccc  
cctggcctcagccccttgacttctcctgcgcgatgaccttgagccccaaaaccttctggctatgcgcatgctg  
gaagagctgaacctgagctataacgggtatcaccactgtgccccgctgccagctccttgacgaatctgagccta  
agccacaccaacatcctggtagctgacccagcagcctcgctggcctgcacagcctgcgagttctctcatggac  
30 gggaactgctactacaagaacctctgcaacggggcggtgaacgtgaccccgagcgccttctgggcttgagcaac  
ctcaccacttgctccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtagctc  
ctgctgtgctcactcactcactgcagctggggcggaagacctgaccaactgacctccttgaatgcttgat  
gtgggtgggaattgcgctcgtgtgatcacgccccacgtctgtacagaatgcggcagaagtccttgatctg  
caccctcagactttccatcacctgagccaccttgaggcctgggtgctgaaggacagttctctccactcgtgaac  
35 tccaagtggttccagggtctggcgaaacctctcggtgctggacctaaagcgagaactttctctacgagagcatcaac  
aaaaccagcgcttctcagaacctgaccgctctgcgcaagctcgacctgtccttcaattactgcaagaaggtagctg  
ttcgcccgctccacctggcaagttccttcaagagcctgggtgtcgtgcgaggagctgaacatgaacggcatcttc  
ttcgcttactcaacaagaacacgctcaggtggctggctggctgtgccaaagctccacacgctgcaccttcaaatg  
aatctcatcaaacaggcgagctcagcgtctttagtaccttccgagccttctgcttggtagctgtccaataat  
40 cgcacagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgaggcggaagggggttccatgg  
cctgcaagtctcaccacgctctcccgagcactccgctctcaaagaacttcatggtaggtgtaagaacctcaga  
ttcaccatggacctgtctcggaacaaccagggtgactatcaagccagagatgttcgtcaacctctccatctccag  
tgtctgagcctgagccacaactgcacgcgaggtgtcaatggctctcagttcctgcccgtgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccttcgaaatcgttcagtgagctcccacagttgcaggcc  
45 ctggacctgagctacaacagccagccattcagcatgcaggggatagggcacaacttcagttttctggccaatctg  
tcagggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggaacgggtgtgggcccgcattgtgggacgaggaggacctttacctctattttctc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaaacctcaac  
tacctccccaaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctctggcc  
50 ttctgccccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcacccctgccta  
ggcagctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttctttgctctggcg  
gtagagctaaaagggtcaacctcagccataaacatcctcaagactgtggatcgctcctgggttggggccattgtg  
atgaacctgacgggtctagacgtgagcagcaacctctgcattgtgcctgcggtgcacctttgtgagacttactg  
ctggaagtgcagaccaagggtgcctggcctggctaacgggtgtgaagtgtggcagctccccgcagctgcaggggccgc  
55 agcatctttgcgcaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggc

- 11 -

## SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVLTALAAALAQGRLPAPFLPCELPQPHGLVNCNWLFLKSVPHFSAAPRANVTSLSLLSNRIH  
HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVLSLS  
RTNIVLDPHTLTGLHALRYLYMDGNCYYKNPCQGALEVVPAGALLGLGNLTHLSLKYNLLEVPRLPPSLETLL  
5 LSYNHIVTLTPEDLANLTALRVLDVGGNCRCDHARNPCRECPKDHKLHSDTFSHLSRLEGLVLKDSLSYNLDT  
RWFGRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRLSLNLSFNYHKKVSFAHLHLAPSFHGLRSLKELDMHGIF  
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR  
NLAPRPLDTRSED FMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
DLSHNKLDLYHGRSFTELPRLALDLSYNSQPFMTQGVGHNL SFVAQLPALRYLSLAHNDIHSRVSQQ LCSASLC  
10 ALDFSGNDLSRMWAEGLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL  
PKLETDL LAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
LKVL DVSANPLHCACGATFVGFLLEVQAAPGLPSRVKCGSPGQLQGH SIFAQDLRLCLDETLSWNCFGISLLAM  
ALGLVVFMLHHL CGWDLWYCFHLCLAWLPHRGQRGADALFYDAFVVF DKAQSAVADWVYNELRVQLEERRGRRA  
LRLCLEERDWLPGKTLFENLWASVYSSRKTFLVLAHTDRVSGLLRASFLLAQORLLED RKDQVVLVILRPDAYRS  
15 RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHNFYNRNFCRGPTTAE

## SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVLTALAAALAQGRLPAPFLPCELPQPHGLVNCNWLFLKSVPHFSAAPRANVTSLSLLSNRIH  
HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVLSLS  
20 RTNIVLDPHTLTGLHALRYLYMDGNCYYKNPCQGALEVVPAGALLGLGNLTHLSLKYNLLEVPRLPPSLETLL  
LSYNHIVTLTPEDLANLTALRVLDVGGNCRCDHARNPCRECPKDHKLHSDTFSHLSRLEGLVLKDSLSYNLDT  
RWFGRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRLSLNLSFNYHKKVSFAHLHLAPSFHGLRSLKELDMHGIF  
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR  
NLAPRPLDTRSED FMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
25 DLSHNKLDLYHGRSFTELPRLALDLSYNSQPFMTQGVGHNL SFVAQLPALRYLSLAHNDIHSRVSQQ LCSASLC  
ALDFSGNDLSRMWAEGLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL  
PKLETDL LAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
LKVL DVSANPLHCACGATFVGFLLEVQAAPGLPSRVKCGSPGQLQGH SIFAQDLRLCLDETLSWNCFG

## 30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttctactgtagctgctgcccggtctgccagccagaccctttggagaagacccccactccctgt  
catgggcccccgctgcacccctgcaccccttctctcctggtgcagggtgacagcgctggctgcggctctggcca  
ggcagggctgctgccttccctgccctgtgagctccagccccacggcctggtgaactgcaactggctcttccctgaa  
gtccgtgccccacttctcgggcgcagcgcggcgcccaacgtcaccagcctctccttactctccaaccgcatcca  
35 ccactgcacgactccgacttcgtccacctgtccagcctacgaactctcaacctcaagtggaaactgccgcggc  
tggcctcagccccatgcacttccctgccacatgaccctcagagcccaacaccttccctggcggcggcggcggc  
ggagctgaacctgagctacaacagcatcacgacgtgcctgcctgcccgactccctcgctgtccctgtcgctgag  
ccgcaccaacatcctggtgctagaccccccacccactcactggcctacatgcctgcgctacctgtacatggatgg  
40 caactgctactacaagaacccctgccagggggcgctggaggtggtgcccgggtgccctcctcggcctgggcaacct  
cacacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgct  
gttgctctacaaccacattgtcaccctgacgctgaggacctggccaatctgactgccctgcgctgcttgatgt  
gggggggaactgccgcggctgtgaccatgcccgcaacccctgcaggaggtgcccgaaggaccaccccaagctgca  
ctctgacaccttcagccacctgagccgctcgaaggcctggtgttgaaagacagttctctacaacctggacac  
caggtgggttcgaggcctggacaggtcccaagtgtgacctgagtgagaaacttctctacgactgcatcaccaa  
45 gaccacggccttcaggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt  
tgcccacctgcacctggcaccctcctttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt  
ccgctcgctcagtgagaccacgctccaacctctgggtccaactgcctatgctccagacctgcccctgcagatgaa  
cttcattaaccaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggaacaaccg  
catcagcggagctgcaaggccagtgccattactagggaggtggatggtagggagagggtctggctgccttccag  
50 gaacctcgctccagctccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcac  
cttggaactgtctcggaacaaactgtgacacatccagtcggagatggttgctcgctctcagcctcgagtcgct  
gcgctgagccacaacagcatctcccaggcggtcaatggctctcagtttgctgcgctgaccagcctgcgggtgct  
ggacctgtccacaacaagctggacctgtatcacggcgctcggttcacggagctgccgcgctggaagcactgga  
cctcagctacaatagccagccctttaccatgcagggtgtggggccacaacctcagcttctggtggccagctgcccgc

- 12 -

cctgcgtacctcagcctggcgacacaatgacatccatagccgagtggtccagcagctctgtagcgcctcactgtg  
 cgccctggacttttagcggcaacgatctgagccggatgtgggtgagggagacctctatctccgcttcttccaagg  
 cctaagaagccttagtctggctggacctgtcccagaaccacctgcacacctctcctgccagtgccctggacaacct  
 ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcct  
 5 gccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac  
 ccagctgcgaggctggacctcagtggaacagcatcggtcttgtgaacctggcttctttgcccctggccaagca  
 gttagaagactcaacctcagcgccaatgccctcaagacagtggagccctcctggtttggctcgatgggtgggcaa  
 cctgaaagctcctagcgtgagcgccaacctctgcactgtgctgtggggcgaccttcgtgggttctctgctgga  
 ggtacaggctgcctgctgggtgcccagccgctcaagtgtggcagtcggggcagctccagggtccatagcat  
 10 ctttgcgcaagacctgcgctctgctggatgagacctctcgtggaactgttttggcatctcgtgctggccat  
 ggccctgggctgggtgtgcccctgctgcaccacctctgcggtgggacctctggtactgcttccacctgtgct  
 ggctgggtgccccaccgagggcagcgcgggggcgagacgcccctgttctatgatgccttcgtggtctttgacaa  
 agctcagagtgtgtggcgcactgggtgtacaacagctgcgggtgcagctggaggagcgccgtggcgccgcgc  
 actgcgctgtgctggaggagcgagactggttacctggcaagacgctcttcgagaacctgtgggctcagctca  
 15 cagcagcgcaagacctgtttgtgctggcccacacggacgctgtcagcgccctcttgcgtgccagtcttctgct  
 ggcccagcagcgctgctggaggaccgcaaggacgttgtagtgctgggtgatcctgcgcccagctccacctgctc  
 ccgctacgtgcggtgcgcccagcgctctgcgcccagagtgtcctcctctggccccaccagccccgtgggcagg  
 cagcttctgggcccagctgggcacagccctgaccagggacaaccaccacttctataaccggaacttctgcccggg  
 cccacgacagccgaatagcactgagtgcagcccagttgccccagccccctggatttgcctctctgctgggg  
 20 tggcccaacctgctttgtcagccacaccactgctctgctccctgttccccacccccccccagcctggcatgt  
 aacatgtgcccataaatgctaccggaggggccaagaaaaaaaaaaaaaaaaaaaaa

## SEQ ID NO:8 (Porcine TLR9)

atgggcccccgctgcacctgcaccccccttctctcctgggtgcaggtgacagcgctggctgcggtctgcccag  
 25 ggcaggctgccttctcctgctgtgagctccagccccacggcctggtgaactgcaactggctcttctcctgaag  
 tccgtgccccacttctcggcgagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatccac  
 cactgcacgactccgacttctgccaacctgtccagcctacgaactctcaacctcaagtggaaactgcccgcggct  
 ggctcagccccatgcacttccctgcccacatgaccatcgagcccaacaccttctcctggcctgcccacctggag  
 30 gagctgaacctgagctacaacagcatcacgaccgtgctgcccctgcccagctccctcgtgtccctgtcgctgagc  
 cgcaccaacatcctggtgctagacccccaccacctcactggcctacatgccctgcgctacctgtacatggatggc  
 aactgctactacaagaacctctgcccagggggcgctggagggtgggtgcccgggtgcccctcctcggcctgggcaacctc  
 acacatctctcactcaagtacaacaatctcagcgaggtgccccgcagcctgccccccagcctggagacctgctg  
 35 ttgtcctacaaccacattgtcacctgacgcctgaggacctggccaatctgactgcccctgcgctgcttgatgtg  
 ggggggaactgcccgcgctgtgaccatgcccgaacctctgcagggagtgcacaaaggaccacccccagctgcac  
 tctgacaccttcagccacctgagccgctcgaaggcctgggtgttgaaagacagttctctctacaacctggacacc  
 aggtggttccgaggcctggacaggtcccaagtgtggacctgagtgagaacttctctacgactgcacaccaag  
 accacggccttccagggcctggcccagctgcgcagcctcaacctgtccttcaattaccacaagaagggtgctctt  
 gcccacctgcacctggcacctcctttgggcacctccggctccctgaaggagctggacatgcatggcatcttcttc  
 cgctcgctcagtgagaccacgctccaacctctggtccaactgcctatgctccagacctgcgctgcagatgaac  
 40 ttcatataaccaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggaacaaccgc  
 atcagcgagctgcaaggccagtgccattactaggagggtggatggtagggagagggtctggctgcttccagg  
 aacctcgctccacgtccactggacactctccgctcagaggacttcatgcccactgcaaggccttcagcttcacc  
 ttggacctgtctcggaacaacctggtgacaatccagtcggagatgtttgtcgcctctcacgcctcgagtgcctg  
 45 cgctgagccacaacagcatctcccaggcggtcaatggctctcagtttgtgcccgtgaccagcctgcgggtgctg  
 gacctgtcccacaacaagctggacctgtatcacggcgctcggttcacggagctgcccgcgctggaagcactggac  
 ctcagctacaatagccagccctttaccatgcagggtgtgggcccacaacctcagcttctggtggccagctgcccgc  
 ctgcgctacctcagcctggcgacaaatgacatccatagcagtggtcccagcagctctgtagcgcctcactgtgc  
 50 gccctggacttttagcggcaacgatctgagccggatgtgggtgagggagacctctatctccgcttcttccaaggc  
 ctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccacgtgcccctggacaacctc  
 cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcctg  
 cccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc  
 cagctgcccaggctggacctcagtggaacagcatcggtcttgtgaacctggcttcttggccctggccaagcag  
 ttagaagactcaacctcagcgccaatgccctcaagacagtggagccctcctgggttggctcgatgggtgggcaac  
 55 gtacaggctgcgctgctgggtgcccagcgctcaagtgtggcagtcggggcagctccaggcccatagcatc  
 tttgcgcaagacctgcgctctgctggatgagacctctcgtggaactgttttggc

- 13 -

## SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELPQHPGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEIPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL  
5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCPRALEVAPGALLGLGNLTHLSLKYNLLEVPRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLYKLEK  
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNHKKVSAHLHLASSFGSLVLEKLDMHGIF  
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAPPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
GLAPGPLDAVSSKDFMPSCNLFNFTLDSRNNLVITIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
10 LSHNKL DLYHGRSFTTELPQLEALDLSYNSQPFMSQGVGHNL SFVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVPIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSANPLHCACGAAFVDLFLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFGLSLLMVA  
LGLAVPMLHHL CGWDLWYCFHLCLAHLP RRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRRRAL  
15 RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLEDKDVVVLVILRPAAYRSR  
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNRHFYNNRNFRCGP TAE

## SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELPQHPGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEIPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL  
20 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCPRALEVAPGALLGLGNLTHLSLKYNLLEVPRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLYKLEK  
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNHKKVSAHLHLASSFGSLVLEKLDMHGIF  
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAPPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
GLAPGPLDAVSSKDFMPSCNLFNFTLDSRNNLVITIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
25 LSHNKL DLYHGRSFTTELPQLEALDLSYNSQPFMSQGVGHNL SFVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVPIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSANPLHCACGAAFVDLFLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG  
30

## SEQ ID NO:11 (Bovine TLR9)

gggaagtgggcgccaagcatccttccctgcagctgcctcccaacctgcccggccagaccctctggagaagccgcat  
tccctgtcatgggcccctactgtgccccgcacccctttctctcctggtgcaggcgccgactggcagcgcc  
tggccgagggcaccctgcctgccttccctgcctgtgagctccagcccatggcaggtggactgcaactggctgt  
35 tccctgaagtctgtgccgcacttttcggctggagcccccgggccaatgtcaccagcctctccttaactccaacc  
gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaactgcc  
cgccggccggcctcagcccatgcacttccccctgcgtatgacctcgagcccaacaccttccctggctgtgccca  
ccctggaggagctgaacctgagctacaacggcatcacgacctgcctgcctgccagttccctcgtgtccctgt  
cgctgagccacaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcccctgcgctttctgtaca  
tggacggcaactactacatgaacccctgcccgcggcctggagtgccccagggccctcctcgccctgg  
40 gcaacctcacgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggaca  
ccctgtgctgtcctacaaccacattgtcacctggcaccgaggacctggccaacctgactgccctgcgcgtgc  
ttgacgtgggtgggaactgccgcgctgcgacctgcccgaacccctgcagggagtgcccaagaacttcccca  
agctgcaccctgacaccttcagtcacctgagccgctcgaaggcctggtgtgaaggacagtctctctacaaac  
45 tagagaaagattggttcgcggcctgggcaggctccaagtgtcgcacctgagtgagaacttccctctatgactaca  
tcaccaagaccaccatcttcaacgacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaagg  
tgtccttcgcccactgcacctagcgtcctccttgggagctggtgtcctggagaagctggacatgcacggca  
tcttcttcgctccctaccaacatcacgctccagtcgctgacccggctgccccagctccagagtctgcatctgc  
agctgaacttcatcaaccaggcccagctcagcatcttggggccttcccagacctgctctcgtggacctgtcgg  
50 acaaccgcatcagcggagccgcgacgccagcggccgcccctgggggaggtggacagcaggggtggaagtctggcgat  
tgcccaggggctcgctccaggcccgtggacgcccgtcagctcaaaggacttcatgccaaagtgcacacctcaact  
tcacctggacctgtcacggaacaacctggtgacaatccagcaagagatgtttaccgcctctccgcctccagt  
gcctgcgcctgagccacaacagcatctcgaggcggttaatggctcccagttcgtgcccgtgaccagcctgcgag

- 14 -

tgctcgacctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgccgcagctggaggcac  
tggaacctcagctacaacagccagcccttcagcatgcagggcggtgggccacaacctcagcttcgtggccagctgc  
cctccctgcgctacctcagccttgccgacaaatggcatccacagccgctgtcacagaagctcagcagcgctcgt  
5 tgcgcgccctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctgctttttca  
aaggcttgaggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggaca  
acctgcccagagcctggggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccg  
tcttgcctggctggaagcctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgcctg  
gcatccggctccagaagctggagctgagcagcaacagcatcggtctcgtgatccccggcttcttctcgcgcga  
10 ctcggtgatagagcttaacctcagcgccaatgcctgaagacagtgatccctcctgggttcggttctcttagcag  
ggacctgaaaaatcctagacgtgagcgccaacccgctccactgcgcctggggggcgccctttgtggaacttctgc  
tgagagagacaggaggcctgcccgggtgtccaggcgctcacatgtggcagtcggggccagctccaggggcgca  
gcatcttcacacaggacctgcgcctctgcctggatgagacctctccttgagctgctttggcctctcactgctaa  
tggtggcgctggcctggcagtgcccatgctgcaccacctctgtggctgggacctctggtactgcttccacctgt  
15 gtctggcccatttgccccgacggcgccggcagcgggcgaggacacctgctctatgatgccgtcgtggtcttcg  
acaaggtgcagagtgcagtggtgatgtgggtgtacaacagctccgcgtgcagctggaggagcgccggggcgcc  
ggcgctccgctctgcctggaggagcgagactggctccctggtaagacgctcttcgagaacctgtgggctcgg  
tctacagcagccgaagacctgttcgtgctggaccacacggaccgggtcagcgccctcctgcgcgccagcttcc  
tgctggcccagcagcgctgttgaggagccgaaggacgtcgtagtgtggtgatcctgcgccccgcgcctatc  
20 ggtcccgctacgtgcggctgcgccagcgctctgcgcagagcgctcctctggccccaccagccagtgggc  
agggtagtcttctgggccaacctgggcatagccctgaccagggaacacctcacttctataaccggaaacttctgcc  
ggggccccacgacagccgaatagcacagagtgaactgccag

## SEQ ID NO:12 (Bovine TLR9)

atggggccctactgtgccccgcacccccctttctctcctgggtgcaggcgccggcactggcagcgccctggccgag  
25 ggcacctgcctgccttccctgacctgcagcccatgggtcaggtggactgcaactggctgttctgaag  
ctgtgctcgcaacttttcggctggagcccccgccgaatgtcaccagcctctccttaatctccaaccgcatccac  
cacttgcatgactctgacttcgtccacctgtccaaacctgcgggtcctcaacctcaagtggaaactcccgcggcc  
ggcctcagccccatgcaacttccctgacctatgaccatcgagcccaacaccttctggctgtgcccacctggag  
30 gagctgaacctgagctacaacggcatcacgacctgacctgacctgcccagttcctcgtgtcctgtgcgtgagc  
cacaccagcatcctgggtgctaggccccacccacttcaccggcctgcacgacctgaccttctgtacatggacggc  
aactgctactacatgaacccctgcccgcgggcccctggagggtggccccaggcgccctcctcggtcgggcaacctc  
acgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggacacctgctg  
35 tctgctcaaccacattgtcacctggcaccggagacctggccaacctgactgacctgacctgacctgacctg  
gggtgggaactgcccgcgtgcgacctgcccgaaccttgcaggagtgccaaagaacttcccaagctgcac  
cctgacaccttcagtcacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa  
gattgggttcgcggcctgggaggtccaagtgtcagctgagtgagaacttctctatgactacatcaccaag  
40 accaccatcttcaacgacctgacctgagctgcgcagactcaacctgtccttcaattaccacaagaagggtgtccttc  
gcccacctgcacctagcgtcctcctttgggagctggtgtccctggagaagctggacatgcacggcatcttcttc  
cgctccctcaccaacatcacgctccagtcgctgacctggctgcccagctccagagctctgcatctgcagctgaac  
45 ttcacacaccaggccagctcagcatctttggggccttcccagcctgctcttcgtggacctgtcggacaaccgc  
atcagcggagccgcgacgcccagcgccgccccggggagggtggacagcagggtggaagtctggcgatgcccagg  
ggcctcgctccaggcccgctggacgacctgacctcaaaggacttcacgccaagctgcaacctcaacttcaccttg  
gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctccgcctccagtgctgcgc  
50 ctgagccacaacagcatctcgagcggttaatggctcccagttcgtgcccgtgaccagcctgcgagtgctcgac  
ctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgccgcagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcgctggggccacaacctcagcttcgtggccagctgcccctcctg  
cgctacctcagcttgcgcacaatggcatccacggcgctgtgtcacagaagctcagcagcgctcgttgcgcgc  
ctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctgtcttctcaaaggcttg  
55 aggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggacaacctgccc  
aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgacctcctgccc  
cggtggaagcctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgcctggcatccgg  
ctccagaagctggacgtgagcagcaacagcatcggtctcgtgatccccggcttcttcgtccgcgcgactcggtg  
atagagcttaacctcagcgccaatgcctgaagacagtggaatccctcctgggttcggttctctagcagggaacctg  
aaaatcctagacgtgagcgccaacctcactgcgcctgcggggcgccctttgtggaacttctgctggagaga  
caggaggcctgcccgggtgtccaggcgctcacatgtggcagtcggggcagctccaggggcgcagcatcttc  
acacaggacctgcgcctcctgctggatgagacctctccttggactgcttggc



- 15 -

## SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELQPHGLVNCNWFLKSVPHFSAAAPRDNVTSLSLLSNRI  
 HHLHDSDFQAQLSNLQKLNKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
 5 SRTNQLQDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL  
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN  
 PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNHYHKKVSFAHLTLAPSFGLSLSLQELDMHGIF  
 FRSLSQKTLQPLARLPLMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGKKVWLTS  
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVPQEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
 10 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMSRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
 WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLLPCTLGNLPKSLQLRLRNNYLAFNWSSLT  
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSII FVVPGFALATRLRELNLSANALRTEEPSWFGFLAG  
 SLEVL DVSANPLHCACGA AFVDFLLQVQA AVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV  
 VALGLAMPMLHHL CGWDLWYCFHLGLAWLPRRGWQRGADALSYDAFVFDKAQSAVADWVYNELRVRLERERRRR  
 15 ALRLCLEERDWLPKTLFENLWASVYSRKMLFVLAHTDQVSGLLRASFLLAQQRILLEDRKDVVVLVILSPDARR  
 SRYVRLRQRLCRQSVLFWPHQPSGQRSFVAQLGMALTRDNRFYFNQFCRGPTMAE

## SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELQPHGLVNCNWFLKSVPHFSAAAPRDNVTSLSLLSNRI  
 20 HHLHDSDFQAQLSNLQKLNKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
 SRTNQLQDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL  
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN  
 PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNHYHKKVSFAHLTLAPSFGLSLSLQELDMHGIF  
 25 FRSLSQKTLQPLARLPLMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGKKVWLTS  
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVPQEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMSRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
 WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLLPCTLGNLPKSLQLRLRNNYLAFNWSSLT  
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSII FVVPGFALATRLRELNLSANALRTEEPSWFGFLAG  
 30 SLEVL DVSANPLHCACGA AFVDFLLQVQA AVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG

## SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgcgtgaagggactgagcagcacaagcattcctcctctgcagctgctgccagtg  
 tgccagctggaccctctggatcatctccactccctgtcatgggccccttgccatggtgcccctgcagcccctgtct  
 ctctgtgctgagcgcccatgctggcgtggtctggcccaggcaccctgcctccctcctgcctgtgagctc  
 35 cagccccagccgctgtgaactgcaactggtctgttccctgaagtccgtgccccacttctcagcagcagcaccgccg  
 gacaatgtcaccagccttccctgtctctcaaccgcatccaccacctccagactccgactttgcccactgtcc  
 aacctgcagaaactcaacctcaaatggaactgcccgcagccgctcagccccatgcacttcccctgccacatg  
 accatcgagcccaacttctcctggctgtacccaccctggaggagctgaacctgagctacaacggcatcacgact  
 gtgcctgcccctgcccagctccctcgtgtccctgatcctgagccgcaccaacatcctgcagctagacccccaccagc  
 40 ctacagggcctgcatgcccctgcgcttccctatacatggatggcaactgctactacaagaacccctgcccgcgggccc  
 ctggagggtggccccaggcgcctccttgccctgggcaacctcaccacctgtcactcaagtacaacaacctcaca  
 acggtgccccgcagcctgccccctagcctggagtacctgtgtgtctacaaccacattgtcacctggcacct  
 gaggacctggccaatctgactgcccctgcgtgtgctcgatgtgggtggaaactgcccgcgctgtgacctgcacgc  
 aacctcgtggtgagtgcccacataaattccccagctgcactccgacaccttcagccacctaaagccgctagaa  
 45 ggcctcgtgttgaaggatagttctctctaccagctgaaccccagatgggtccctggcctgggcaacctcacagtg  
 ctgacctgagtgagaacttccctctacgactgcataccaaaaccaaggcattccagggcctggcccagctgcga  
 agactcaacttgtccttcaattaccataagaaggtgtccttcgcccacctgacgctggcaccctccttcgggagc  
 ctgctctccctgcaggaactggacatgcattgctcttccgctcactcagccagaagacgctccagccactg  
 gccgcctgcccctgctccagcgtctgtatctgcagatgaactcatcaaccaggcccagctcggcatcttcaag  
 50 gcttccctggctcgtcgtacatagacctgtcagacaacgcacatcagtgagctgtggagcgggtggccaccaca  
 ggggaggtggatgggtgggaagaaggtctggctgacatccaggacacctcactccagggccactggacccccagc  
 tctgaggacttcatgccaagctgcaagaacctcagcttcaccttggacctgtcacggaacaacctggtaacagtc  
 cagccagagatgtttgcccagctctcgcgcctccagtgcctgcgctgagccacaacagcatctcgaggcggctc

- 16 -

aatggctcacagttcgtgccactgaccagcctgcaggtgctggacctgtccataacaaactggacctgtacat  
ggcgctcgtttacggagctgccgagctggaggccctggacctcagctacaacagccagcccttcagcatgcgg  
gggtggggccacaacctcagcttctgtggccagctgccaccctgcgctacctcagcctggcacacaatggcatc  
cacagccgtgtgtcccagcagctctgcagcactcgctgtgggcccctggacttcagcggcaattccctgagccag  
5 atgtgggctgagggagacctctatctccgcttcttccaaggcctgagaagcctaataccggctagacctgtccag  
aatcgtctgcataacctcctgccatgcacctgggcaacctccccaagagcttgacgtgctgcgtctccgtaac  
aattacctggccttcttcaattggagcagcctgacctcctgcccaacctggaaacctggacctggctggaaac  
cagctgaaggctctgagcaatggcagcctgccttctggcaccagctccagaggctggacgtcagcaggaacagc  
atcatcttcgtggtccctggcttcttctgtctggccacgaggctgcgagagctcaacctcagtgccaacgcctc  
10 aggacagaggagccctcctgggttgggttctctagcaggtcccttgaagtcttagatgtgagcgccaacctctg  
cactgcgctgtggggcagccttctgtgacttctgtgcagggttcaggctgccgtgcttggctgtgccagccgc  
gtcaagtgtggcagtcggggccagctccagggccgcagcatcttcgcacaagacctgcgctctgctggacaag  
tccctctcctgggactgttttggctctctcattgctggttgtggccctgggctggccatgcctatgttgaccac  
ctctgcggctgggacctctggactgcttccacctgggctggcctggctgccccggcgggggtggcagcggggc  
15 gggatgcctgagctatgatgccttctgtggtcttcgacaaggcacagagcgcagtgccgactgggtgtacaat  
gaactgcgggtgcggctagaggagcgcgtggggcgccgctccgctgtgtctggaggagcgtgacgtgta  
cctggcaagacgtgttgcgaaaacctgtgggctcagctacagcagccgcaagatgctgttctgtctggccac  
acggaccaggtcagtgccctcttgcgtgccagcttctgtgcccagcagcgtctgtggaggaccgcaaggac  
gttgtggtgctggtaatcctgagccctgacgcccgcgttcccgctacgtgcggctgcgccagcgcctctgcgc  
20 cagagtgtcctctctggccccaccagcctagtggccagcgcagcttctggggccagctaggcatggccctgacc  
agggacaaccgccaactctataaccagaacttctgcggggcccgacgatggctgagtagcacagagtgcagcc  
tggcatgtacaacccccagccctgaccttgccctctctgcctatgatgccagctgctgctcactctgtgacgccc  
tgctctgcctccgcacctcaccctggcatacagcaggcactcaataaatgccactggcaggccaaacagcca  
aaaaaaaaaaaaaaaa

25

## SEQ ID NO:16 (Equine TLR9)

atgggccccttgccatgggtgcctgcagcccctgtctctcctgggtgcaggcgcccatgctggcctggctctggcc  
caaggcacccctgcctcccttctgcctgtgagctccagcccccagggcctggtgaactgcaactggctgttctg  
aagtccgtgcccacttctcagcagcagcaccgccggacaatgtcaccagccttctctgtctccaaaccgcatc  
30 caccacctccagcactccgacttgcaccaactgtccaacctgcagaaactcaacctcaaatggaactgcccgcga  
gcccgcctcagcccatgcacttccctgccacatgaccatcgagcccaacacttctctggctgtaccacacctg  
gaggagctgaacctgagctacaacggcatcacgactgtgctgcccctgccagctccctcgtgtccctgatcctg  
agccgcaccaacatcctgcagctagaccccaccagcctcagggcctgcagcctgccttccctatcatggat  
ggcaactgctactacaagaacctcgcggcgggccctggagggtggccccagggcgcctccttggcctgggcaac  
35 ctacccacctgtcactcaagtacaacaacctcacaacgggtgccccgcagcctgccccctagcctggagtacctg  
ctgttctctacaaccacattgtcacctggcactgaggacctggccaatctgactgcccctgcgtgtgctcgat  
gtgggtggaactgcccgcgctgtgacctgcacgcaacctgcgtggagtggccacataaatccccagctg  
cactccgacaccttcagccacctaaagccgctagaaggcctcgtgttgaaggatagttctctctaccagctgaac  
cccagatggttccgtggcctgggcaacctcacagtgtcgacctgagtgagaacttctctacgactgcacacc  
40 aaaaccaaggcatccagggcctggccagctgcgaagactcaacttgccttcaattaccataagaagggtgtcc  
ttcgccacctgacgtggcaccctccttcgggagcctgctctccctgcaggaactggacatgcattggcatcttc  
ttccgctcactcagccagaagacgtccagccactggccgcctgcccctgctccagcgtctgtatctgcagatg  
aacttcatcaaccaggccagctcgcatcttcaaggacttccctggctgcgctacatagacctgtcagacaac  
cgcacagtgaggctgtggagccgtggccaccacaggggaggtggatgggtgggaagaaggctcgtgcatcc  
45 agggacctcactccagggccactggacacccccagctctgaggacttcagccaagctgcaagaacctcagcttc  
accttggacctgtcacggaacaacctggtaacagctccagccagagatgttggccagctctcgcgctccagtg  
ctgcgctgagccacaacagcatctgcagggcgtcaatggctcacagttcgtgcccactgaccagcctgcaggtg  
ctggacctgtccataaacaactggacctgtaccatgggcgctcgtttacggagctgcccgcagctggaggccctg  
gacctcagctacaacagccagcccttcagcatgcgggtgtggggccacaacctcagcttctgtggccagctgccc  
50 acctgcgctacctcagcctggcacacaatggcatccacagccgtgtgtcccagcagctctgcagcactcgctg  
tgggcccctggacttcagcggcaattccctgagccagatgtgggtgagggagacctctatctccgcttcttccaa  
ggcctgagaagcctaataccggctagacctgtcccagaatcgtctgcataacctcctgccatgcacctgggcaac  
ctccccaagagcttgacgtgctgcgtctccgtaacaattacctggccttcttcaattggagcagcctgacctc  
ctgcccacacctggaaacctggacctggctggaaaccagctgaaggctctgagcaatggcagcctgcctctggc  
55 accgctccagaggctggacgtcagcaggaacagcatcttctgggtccctggccttcttgcctggccacg  
aggctgcgagagctcaacctcagtgccaacgcctcaggacagaggagccctcctgggttgggttctctagcaggc  
tcccttgaagtcttagatgtgagcgccaacctctgcactgcgctgtggggcagccttctgtgacttctgctg

- 17 -

caggttcaggtgcccgtgcccgtgcccagccgctcaagtgtggcagtcggggccagctccagggccgcagc  
atcttcgcacaagacctgcccctctgcccggacaagtcctctctctgggactgttttgggt

## SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELPQPRGKVN CNWFLKSVPRFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL  
RTSILVLGPHTFTGLHALRFLYMDGNCYYKNPCQQA VEVAPGALLGLGNLTHLSLKYNNTLTPRRRLPPSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDS SLYKLEK  
10 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFN YHKKVSFAHLQLAPSF GGLVSLKLDMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWPR  
GLAPGPLAAVSAKDFMPSCNLFNTLDSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNL SFVAQLPSLRYL SLAHNGIHSRVSQKLSSASLRA  
15 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNLAF FNWSSLTVLP  
QLEALDLAGNQLKALSNGSLPPGTRQLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETL  
NILDV SANPLHCACGA AFVDFLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFGFSLLMVA  
LGLAVPMLHHL CGWDLWYCFHLCLAHLP RRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRGRAL  
RLCLEERDWLP GKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILRPAAYRSR  
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNRRHFYNRNFCRGPTTAE

## 20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELPQPRGKVN CNWFLKSVPRFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL  
RTSILVLGPHTFTGLHALRFLYMDGNCYYKNPCQQA VEVAPGALLGLGNLTHLSLKYNNTLTPRRRLPPSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDS SLYKLEK  
25 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFN YHKKVSFAHLQLAPSF GGLVSLKLDMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWPR  
GLAPGPLAAVSAKDFMPSCNLFNTLDSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNL SFVAQLPSLRYL SLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNLAF FNWSSLTVLP  
30 QLEALDLAGNQLKALSNGSLPPGTRQLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETL  
NILDV SANPLHCACGA AFVDFLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFG

## SEQ ID NO:19 (Ovine TLR9)

gtcggcacgggaagtgagcgccaagcatccttccctgcagctgcccggccaacttgcccggccagaccctctggaga  
35 agccgcattccctgccatgggcccctactgtgccccgaccccccttctctcctgggtgcaggcgccgctggc  
agcagccctggcccaggccaccctgcctgccttccctgccctgtgagctccagccccggggaagtgaactgcaa  
ctggctgttccctgaagtctgtgcgcgcttttcggccggagcccccgggccaatgtcaccagcctctccttaat  
ctccaaccgcattccaccacttgacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagt  
40 gaactgcccgcggcgccgctcagccccatgcacttccctgcccgcattgacctcgagcccaacaccttccctggc  
tgtgcccaccctggaggagctgaacctgagctacaatggcatcacgaccgtgcctgcccagttctctcgt  
atccctgtcgtgagccgcaccagcatcctgggtgctaggccccaccacttcaccggcctgcacgcctgcgctt  
ctgtacatggagcccaactgctactataagaaccttgcagcaggccgtggaggtggccccaggcgccctcct  
tggcctgggcaacctcacgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcctgccccccag  
cctggacaccctgctgctgtcctacaaccacatcatcaccctggcaccgaggacctggccaatctgactgcct  
45 gcgtgtgcttgatgtgggcggaactgccgcgctgcgaccacgcccgaacctgaggggagtgccaaagaa  
cttccccaaagctgcaccctgacaccttcagccacctgagccgctcgaaggctgggtgtgaaggacagttctct  
ctacaaactagagaaagactggttcgcggcctgggagagctccaagtgtcgacctgagtgagaacttccctcta  
tgactacatcaccaagaccacctcttcaggaacctgaccagctgcgcagactcaacctgtccttcaattacca  
caagaaggtgtccttcgcccacctgcaactggcaccctcctttggggcctgggtgtccctggagagctggacat  
50 gcacggcatcttcttcgctccctcaccaaccacgctccggccgctgaccagctgcccagctccagagctct  
gagctgtcagctgaacttcatcaaccaggccgagctcagcatctttggggccttcccagcctgctcttctgga  
cctgtcggacaaccgcattcagcggagctgcgaggccggtggccgcccctcggggaggtggacagcgggtggaagt  
ctggcggtggcccaggggcctcgctccaggcccgctggccgcgctcagcgcaaaggacttcatgccaagctgcaa

- 18 -

cctcaacttcaccttggacctgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctccc  
 cctccagtgcctgcgctgagccacaacagcatctcgaggcggttaatggctcgagttcgtgccgctgaccg  
 cctgcgagtgtcgacctgtcctacaacaagctggacctgtaccatgggcgctcggttcacggagctgccgcagct  
 ggaggcaactggacctcagctacaacagccagcccttcagcatgcaggcgctgggcccacaacctcagcttcgtggc  
 5 ccagctgccgtccctgcgctacctcagccttgcgcacaacggcatccacagccgctgtcacagaagctcagcag  
 cgctcgctgcgcgccctggacttcagcggcaactccctgagccagatgtgggcccaggaggacctctatctctg  
 ctcttcaaaggcttgaggaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgta  
 cctggataaacctgcccagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcag  
 cctgactgttctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcct  
 10 gccacctggcaccggctccagaagctggacgtgagcagcaacagcatcggtttgtgaccttggtctcttctgt  
 ccttgccaaccggctgaaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctgggttcggtcg  
 cttaacagagacctgaatatcctagacgtgagcgccaaccgcctccactgtgcctgcggggcgcccttctgga  
 ctctcctgctggagatgcaggcgccgctgcctgggtgtccaggcgctcacgtgtggcagtcggggccagctcca  
 gggcgcgacgatcttcgcacaggacctgcgctcctgctggatgagacctctccttggaactgcttgggtctctc  
 15 gctgctaactgggtggcgctgggctggcctgctgctgacacctctgtggtcgggacctgtggtactgctt  
 ccacctgtgtctggccatttgcctcgacggcgggcgagcgggcgaggacacctgctcactgaccttctgt  
 ggtcttcgacaaggcgagagtgacgtggcgactgggtgtacaacgagctccgctgcagctggaggagcgccg  
 cgggcgccggcgctccgctctgcctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg  
 ggctcggtctacagcagccgtaagacctgttctgtgctggaccacacggaccgggtcagtggtcctcctgcgcgc  
 20 cagcttctcgtggtggccagcagcgctgttggaggaccgcaaggatgtcgtggtgctggtgatcctgcgccccgc  
 cgctaccgggtccgctacgtgcggctgcgcagcgctctgcgcagagcgtcctcctctggccccaccagcc  
 cagtgggccagggtagcttctgggccaacctgggcatggcctgaccagggacaaccggcacttctataaccggaa  
 ctctgcgggggccccacgacagccgaatagcacagagtgactgcccag

25 SEQ ID NO:20 (Ovine TLR9)

atgggcccctactgtgccccgcaccccccttctctcctgggtgaggcgggcgctggcagcagccctggccag  
 ggcacctgctgccttctgcctgtgagctccagccccgggtaagggtgaactgcaactggctgttctgaag  
 tctgtgccgctgttctcgccggagcccccgggccaatgtcaccagcctctccttaactctcaaccgcatccac  
 30 cacttgcagactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgccgcggcc  
 ggctcagcccatgcacttccccctgcgcgatgaccatcgagcccaacacctcctgggtgtgcccacctggag  
 gagctgaacctgagctacaatggcatcacgacctgcctgcctgcccagttctctcgatccctgtcgctgagc  
 cgcaccagctcctgggtgctaggccccaccacttcacggcctgcacgcctgcgcttctgtacatggacggc  
 aactgctactataagaacccctgccagcaggcggtggaggtggccccaggcgccctccttggcctggcaacctc  
 35 acgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggacacctgctg  
 ctgtcctacaaccacatcatcaccctggcaccggaggacctggccaatctgactgcctgctgtgcttgatgtg  
 ggcggaactgcccgcgctgcgaccacgcccgaacccctgcaggagtgccaaagaacttccccagctgcac  
 cctgacaccttcagccacctgagccgctcgaaggcctggtgttgaggacagttctctctacaaactagagaaa  
 gactgggtccgcggcctgggcaggctccaagtgtcgcactgagtgagaacttctctatgactacatcaccaag  
 accaccatcttcaggaacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaaggtgtccttc  
 40 gccacctgcaactggcaccctccttgggggctggtgtccctggagaagctggacatgcacggcatcttcttc  
 cgctcctcaccaacaccacgctccggcgctgaccagctgcccagctccagagctctgagctctgcagctgaac  
 ttcatcaaccaggccgagctcagcatcttggggccttcccagacctgctcttctgtggacctgtcggacaaccgc  
 atcagcggagctgcgaggccggtggccgcctcggggaggtggacagcggggtggaagtctggcggtggccagg  
 ggctcgtccaggcccgctggccgcgctcagcgcaaggacttcatgccaagctgcaacctcaacttcaccttg  
 45 gacctgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctccgcctccagtgcctgcgc  
 ctgagccacaacagcatctcgaggcggttaatggctcgagttcgtgcgctgacctgcctgagagtgctgcac  
 ctgtcctacaacaagctggacctgtacctgggcgctcgttcacggagctgcccagctggaggcactggacctc  
 agctacaacagccagcccttcagcatgcaggcggtgggcccacaacctcagcttctggggccagctgcgctcctg  
 cgctacctcagccttgcgcacaacggcatccacagcccgctgtcacagaagctcagcagcgctcgtgcgcgcc  
 50 ctggacttcagcggcaactcctgagccagatgtgggcccaggaggacctctatctctgtcttctcaaaggcttg  
 aggaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgtcacctggataacctgccc  
 aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc  
 cagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcctgccacctggcaccgg  
 55 ctccagaagctggagctgagcagcaacagctggcttctgtgacctgtgaccttctggttcggtcgttaacagagacctg  
 aaagagcttaacctcagcgccaacgcctgaagacagtggaaccttctggttcggtcgttaacagagacctg  
 aatatcctagacgtgagcgccaaccgcctccactgtgcctgcggggcgcccttctgtggacttctgtggagatg

- 19 -

caggcgccgctgacctgggctgtccaggcgctcacgtgtggcagtcggggccagctccaggcgccgagcatcttc  
gcacaggacctgcgctctgctggatgagaccctctccttgactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are  
publicly available. For example, an amino acid sequence for canine TLR9 is available as  
GenBank accession number BAC65192 and its corresponding nucleotide sequence is  
available as GenBank accession number AB104899. An amino acid sequence for feline  
TLR9 is available as GenBank accession number AAN15751 and its corresponding  
nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also  
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of canine TLR9  
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively  
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide  
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides  
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-  
822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See  
Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular  
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline  
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID  
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID  
NO:25.

30

#### SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLVQAAALALALAQGTLPALFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI  
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVLSL  
SRTNILLVDPATLAGLYALRFLFLDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL

- 20 -

LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFQQLHPNTFGHLSHLEGLVLRDSSLYSLD  
PRWFHGLGNLMVLDLSENFLYDCITTKAFYGLARLRRLNLSFNHKKVSFAHLHLASSFGSLLSLQELDIHGIF  
FRSLSKTTQLSLAHLPMQLRLHLQLNFI SQAQLSIFGAFGLRYVDLSDNRISGAAEPAAATGEVEADCGERVWP  
QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
5 RVLDSLHNKLDLYHGRSFTLPRLEALDLSYNSQPFMSMRGVGHNL SFVAQLPALRYLSLAHNGIHSRVSQQLRSA  
SLRALDFSGNTLSQMWAEGLDLYLRFFQGLRSLVQLDLSQNLRLHTLLPRNLDNLPKSLRLLRLRDNLYLAFFNWSSL  
ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL  
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFSLSL  
LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRRGVDALEYDAFVVFDKAQSSVADWVYNELRVQLEERRG  
10 RRALRLCLEERDWVPGKTLFENLWASVYSSRKTFLVLRARTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILCPDA  
HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNRHFNQNFRCRGPTTA

## SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQTLPAPFLPCELQPHGLVNCNWLFLKSVPFRFSAAAPRGNVTSLSLYSNRI  
15 HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSSLVSLSL  
SRTNIVLDPATLAGLYALRFLFDLGNCCYKNPCQALQVAPGALLGLGNLTHLSLKYNNTLVVPRGLPPSLEYL  
LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFQQLHPNTFGHLSHLEGLVLRDSSLYSLD  
PRWFHGLGNLMVLDLSENFLYDCITTKAFYGLARLRRLNLSFNHKKVSFAHLHLASSFGSLLSLQELDIHGIF  
FRSLSKTTQLSLAHLPMQLRLHLQLNFI SQAQLSIFGAFGLRYVDLSDNRISGAAEPAAATGEVEADCGERVWP  
20 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
RVLDSLHNKLDLYHGRSFTLPRLEALDLSYNSQPFMSMRGVGHNL SFVAQLPALRYLSLAHNGIHSRVSQQLRSA  
SLRALDFSGNTLSQMWAEGLDLYLRFFQGLRSLVQLDLSQNLRLHTLLPRNLDNLPKSLRLLRLRDNLYLAFFNWSSL  
ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL  
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCF S  
25

## SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttctcgtcagctgctgcccagcctgccagccagaccctctggagaag  
ccccgcctccctgtcatgggcccctgcccgtggcgccctgcaccccctgtctctcctggtgcaggtgcgcgcgta  
gcccgtggccctggcccagggcaccctgcccgtgcccgtgagctccagcccatggcctggtgactgc  
30 aactggctgttctcctcaagtcctgccccgcttctcggcagctgcaccccgcggtaacgtcaccagccttctcctg  
tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccacctgcggcgctcctcaatctcaag  
tggaactgcccgcgcgcagcctcagcccatgcactttccctgtcacatgaccattgagcccaacaccttccctg  
gctgtgcccaccctagaggacctgaatctgagctataacagcatcacgactgtgcccgccttgcaggttcgctt  
gtgtccctgtccctgagccgcaccaacatcctggtgctggaccctgccaccctggcaggcctttatgcccgtgcgc  
35 ttcctgttctggatggcaactgctactacaagaacccctgccagcaggccctgcaggtggcccaggtgccttc  
ctggcctggcgcaacctcacacacctgtcactcaagtacaacaacctcacctggtgcccgcggcgccccc  
agcctggagtacctgtcttctcctacaaccacatcatcaccctggcacctgaggacctggccaatctgactgcc  
ctgctgtcctcgatgtgggtgggaactgtcgccgctgtgaccatgcccgtaacccctgcaggagtgccccaag  
ggcttccccagctgcaccccaacaccttccggccacctgagccacctcgaaggcctggtgttgaggagacagctct  
40 ctctacagcctggaccccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttccctg  
tatgactgcatcaccaaaaccaaagccttctacggcctggcccggtgcgcagactcaacctgtccttcaattat  
cataagaaggtgtcctttgcccacctgcatctggcatcctcctctcgggagcctactgtccctgcaggagctggac  
atacatggcatcttctccgctcgctcagcaagaccacgctccagtcgctggccacctgcccactgtccagcgt  
ctgcatctgcagttgaactttatcagccaggccagctcagcatcttcggcgccctccctggactgscggtacgtg  
45 gacttgtcagacaaccgcatcagtgagctgcagagcccgcggtgccacaggggaggtagaggcagactgtggg  
gagagagtctggccacagtcccgggaccttgcctgtgggcccactgggcaaccccggtcagaggccttcatgccg  
agctgcaggacctcaacttcaccttggaacctgtctcggaacaacctagtactgttcagccggagatgtttgtc  
cggtggcgcgccctccagtgccctgggctgagccacaacagcatctcgaggcggtcaatggctcgagttcgtg  
cctctgagcaacctgcccgtgctggacctgtcccataacaagctggacctgtaccagggcgctcgttcacggag  
50 ctgcccgcgtggaggccttgacctcagctacaacagccagccctcagcatgcccggcggtgggcccacatctc  
agctttgtggcacagctgccagccctgcctacactcagcctggcgccacaatggcatccacgcgcgtgtccag  
cagctccgcagcgccctcgctccgggcccctggacttcagtggaataacctgagccagatgtggggcggtgggagac  
ctctatctccgcttcttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgccctgcataccctc  
ctgccacgcaacctggacaacctccccaaagacgtcgggctcctgcggctccgtgacaattacctggcttcttc  
55 aactggagcagcctggccctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagc

- 21 -

aatggcagcttggcccaacggcacccagctccagaggctggacctcagcggcaacagcatcggtctcgtgggtccc  
agcttttttgccctggccgtgaggcttcgagagctcaacctcagcggcaacgccctcaagacggtggagccctcc  
tggtttgggtccctggcgggtgcccgtgaaagtcttagacgtgaccggcaaccccttgcatctgcgtctgcggcgca  
accttcgtggacttcttgctggaggtgcaggctgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccg  
5 ggccagctccagggccgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgt  
ttcagcctctcgtgctggtgctggtgcccctgagcctggctgtgcccattgctgcaccagctctgtggctgggacctc  
tggtactgcttcacattgctgctggctggtgctgcccggcgggcgggcggggtgtggatgccctggcctat  
gacgccttcgtgggtcttcgacaaggcgacagctcggtgcgggaggggtgtacaatgagctcggggtacagcta  
gaggagcgcggtgggcgcggggcgctacgcctgtgtctggaggaaacgtgactgggtaccgggcaaaacccctcttc  
10 gagaacctctgggcctcagtttacagcagcggcaagacgctgtttgtgctggccgcacggacagagtcagcggc  
ctcctgcgtgccagcttctctgctggcccaacagcgcctgctggaggaccgcaaggacgctcgtggtgctggtgatc  
ctgtgccccgacgcccaccgctcccgcctatgtgcggtgcgccagcgcctctgcgcagagtgctcctcctctgg  
ccccaccagcccagtgggccagcgcagcttctgggcccagctgggcacggccctgaccagggacaacggccacttc  
tacaaacgaactctgcgcggggccccacgacgcctgtaggcagacagcccagcaccttcgcgcgccctacacc  
15 tgcctgctgtctgggatgcgcagctctgtggctctacaccgcgcgctctgtctcccctacaccagccctggca  
taaagcgaccgctcaataaatgctgctggtagac

SEQ ID NO:24 (Canine TLR9)

atgggcccttgccgtggcgccctgcacccctgtctctcctgggtgaggctgccgcgtagccctggccctggcc  
20 cagggcaccctgcttgcccttctgacctgtgagctccagcccatggcctggtgaactgcaactggctgttctc  
aagtccgtgccccgttctcggcagctgcaccccgcgtaacgtcaccagccttctctgtactccaaccgcac  
caccacctccatgactatgaactttgtccacttcgtccacctgccggcgcttcaatctcaagtggaaactgccgcgc  
gccagcctcagccccatgcactttctctgtcacatgaccattgagcccaacaccttctctggctgtgccaccct  
gaggacctgaattctgagctataacagcatcacgactgtgccccctgccagttctgctgtctctgtccct  
25 agccgcaccaacatcctgggtgctggacctgccacctggcaggcctttatgccctgcgcttctctgttctctggat  
ggcaactgctactacaagaacccctgccagcaggccctgcagggtggccccagggtgccctctctgggctgggcaac  
ctcacacacctgtcactcaagtacaacaacctcacctgggtgccgcggggcctgccccccagcctggagtaacctg  
ctcttgtctacaaccacatcatcacctggcacctgaggacctggccaatctgactgccctgcgtgtctctgat  
gtgggtgggaactgtgcgcgtgtgacctagccctgaacccctgcaggagtgcccccaagggtcttccccagctg  
30 caccacaacaccttcggccacctgagccacctcgaaggctcgtgtgtgaggacagctctctctacagctcggac  
ccagggtgggttccatggcctgggcaacctcatgggtgtggacctgagtggagaacttctctgtatgactgcatcacc  
aaaaccaaaagccttctacggcctggcccggtgcgagactcaacctgtccttcaattatcataagaagggtgtcc  
tttggccacctgcatctggcatcctccttcgggagcctactgtccttgaggagctggacatacatggcatcttc  
ttcgcctcgctcagcaagaccacgctccagtcgctggcccaacctgcccatgctccagcgtctgcatctgcagttg  
35 aactttatcagccaggccagctcagcatcttcggcgcccttccctggactgcggtacgtggacttgtcagacaac  
cgcactcagtgagctgcagagcccggtgcacagggaggtagaggcagactgtggggagagagctctggcca  
cagtcccggaacctgtctctgggccactgggcaccccgctcagaggccttcattggcagactgcaggaccctc  
aacttcaccttggacctgtctcggaacaacctagtgactgttcagccggagatgtttgtccggttggcgcgctc  
cagtgcctgggcctgagccacaacagcatctcgcaggcggtcaatggctcgcagttcgtgacctgagcaacctg  
40 cgggtgctggacctgtcccataacaagctggacctgtaccaaggcgctcgttcacggagctgccgcggctggag  
gccttggacctcagctacaacagccagcccttcagcatgcggggcggtgggcacaaatctcagcttttgtggcacag  
ctggcagccctgcgctacctcagcctggcgcaaatggcatccacagccgcgtgtccagcagctccgcagcgcc  
tcgctccggccctggacttcagtggaataacctgagccagatgtgggcgagaggacacctctatctccgcttc  
ttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgctctgataacctctctgcacgcaacctg  
45 gacaacctcccaagagcctgcggctcctgcggctccgtgacaattacctggctttcttcaactggagcagcctg  
gcctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc  
aacggcaccacgctccagaggctggacctcagcggaacagcatcggcttcgtgggtcccagcttttttgccctg  
gccgtgaggcttcgagagctcaacctcagcgccaacgccctcaagacggtggagccctcctggtttggttcctg  
gcgggtgcctgaaagtctagacgtgaccggcaaccccttcgattgcgcttgccggcgcaacctctctggacttc  
50 tctggaggtgcaggctgcggtgcggcctgcctgacgctgtcaagtgccgagccggcgccagctccagggc  
cgagcatctcgcacaggacctgcgcctctgcctggacgaagcgtctctctgggtctgtttcaagc

SEQ ID NO:25 (Feline TLR9)

55 MGPCHGALHPLSLLVQAAALAVALAQGTLPAPFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI  
HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLSVLSL

- 22 -

SRTNIIVLDPANLAGLHSLRFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLNHLLEGLVLKDSLSYNLN  
 PRWFHALGNLMVLDLSENFLYDCITKTTFQGLAQLRRLNLSFNHKKVSFAHLHLAPSGSLLSLQQLDMHGIF  
 FRSLSETTLRSLVHLPMQLSLHLMNFINQAQLSIFGAFFGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS  
 5 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGSRFTLPRLEALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNLRLHTLLPRTLNDLPLKSLRLLRLRDNLYLAFFNWSSLV  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLNANALKTVEPSWFGSLAG  
 TLKVLDVTGNPLHCACGAADFVDFLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGLSLLT  
 10 VALGLAVPMLHHLCGWDLWYCFHLCLAWLPRRGRRRGADALPYDAFVFDKAQSAVADWVYNELRVRLERRRGR  
 ALRLCLEERDWPGLKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPDAHR  
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFRCRGPPTAE

## SEQ ID NO:26 (Feline TLR9)

MGPCHGALHPLSLVQAAALAVALAQGTLPAPFLPCELQRHGLVNCDWLFLKSVPHFSAAPRGNVTSLSLYSNRI  
 HHLHDSDFVHLSLRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSSLVSLSL  
 SRTNIIVLDPANLAGLHSLRFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLNHLLEGLVLKDSLSYNLN  
 PRWFHALGNLMVLDLSENFLYDCITKTTFQGLAQLRRLNLSFNHKKVSFAHLHLAPSGSLLSLQQLDMHGIF  
 20 FRSLSETTLRSLVHLPMQLSLHLMNFINQAQLSIFGAFFGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS  
 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGSRFTLPRLEALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNLRLHTLLPRTLNDLPLKSLRLLRLRDNLYLAFFNWSSLV  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLNANALKTVEPSWFGSLAG  
 25 TLKVLDVTGNPLHCACGAADFVDFLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG

## SEQ ID NO:27 (Feline TLR9)

agggctctgcgagctccaggcattctctctgcccctgctgcccagctctgcccacccctctggagaagcccc  
 cactccctgtcatgggcccctgcccagctgcccctgctctctctggtgcaggtgcccgcgtggcgcg  
 30 tggccctggcccagggcaccctgctgcccctgctgagctccagcgccacggcctggtaattgctgact  
 ggctgttctcaagtccgtgcccacttctcgccggcagcgcccctggttaacgtcaccagcttctccctgtact  
 ccaaccgcatccaccacctccagcactccgacttctgcccactgtccagcctgcggcgtctcaacctcaaatgga  
 actgcccacccgcccagcctcagcccctgcaacttccctgtcacatgaccattgagccccacaccttctggcgcg  
 tgcccacccctggaggagctgaacctgagctacaacagcatcacgacagtaccgcccctgcccagttccctcgtgt  
 35 cctgtccttgagccgtaccaacatcctggtgctggaccctgccaacctcgagggtgcaactcctctgccccttct  
 tgttctctggatggcaactgctactacaagaacccctgcccgcaggccctgcaggtggccccgggcccctccttg  
 gcccgggcaaccttacgcacctgtcactcaagtacaacacactcactgcggtgcccgcggcctgccccagcc  
 tggagtacctgctattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgcccctgc  
 gtgtgctcgatgtgggtgggaactgccgtcgctgtgaccacgcccgaacccctgtatggagtggcccaagggct  
 40 tcccgcacctgcacctgacaccttcagccacctgaaccacctcgaaggcctggtgtgaaggacagctctctct  
 acaacctgaacccagatggttccatgcccctgggcaacctcatggtgctggacctgagtgagaacttccatata  
 actgcatcaccaaaaccacagccttccaggccctggcccagctgcgcagactcaacttgtcttcaattaccaca  
 agaaggtgtccttggcccactgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatgc  
 atggcatcttctccgctcgctcagcgagaccagctccggctcgctggctccacctgcccagctgctccagagctgc  
 45 acctgcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc  
 tgtcagacaaccgcataagtggagccatggagctggcggtgccacgggggaggtggatggtggggagagagtc  
 ggctgccatctggggacctagctctggggccaccgggcacccctagctccgagggttcatgccaggctgcaaga  
 ccctcaacttcaacttggacctgtcacggaacaacctagtgaacatccagccagagatgttggccggctctcgc  
 gcctccagtgctgctcctgagccgcaacagcatctcgaggcagtcacaggctcacaatttatgcgctgacca  
 50 gcctgcaggtgctggacctgtccataacaagctggacctgtaccatggcgctcttccaggagctgcgcgggc  
 tggaggccctggacctcagctacaacagccagccctcagatgcagggcggtgggtcacaacctcagcttctgtg  
 cacagctgcggccgctcgctatctcagcctggcgccacacagcatccacagccgtgtgtccagcagctgtga  
 gcgcctcgctgcgggccttggacttcagcggcaatgcttgcggcgatgtggggcggaggagacctgtatctcc  
 acttcttccgaggcctgaggagcctggtccggttgatctgtcccagaatcgccctgcataccctcttgcacgca  
 55 cctggacaacctccccagagcctgcccgtgctgcgtctccgtgacaattatctggcttcttcaactggagca



- 23 -

gcttggtcctcctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagct  
 tgcctaattggaaccagctccagaggtggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg  
 ctctggccaccaggtgctgagagctcaacctcagtgccaacgcctcaagacgggtggagccctcctgggttcggtt  
 ctctagcgggcaacctgaaagtcttagatgtgactggcaacccctgcaactgcgctgtggggcgcccttcgtgg  
 5 acttcttctgtggaggtgcaggtgcagtgcccggtgccaggccacgtcaagtgtggcagtcagggtcagctcc  
 agggcgcgagcatctttgctcaggatctgctgctctgctggatgaggccctctcctgggactgttttggcctct  
 cgctgctgaccgtggccctgggctggcgtgcccattgctgcaccacctctgtggctgggacctctgggtactgct  
 tccacctgtgctggcctggctgccccggcgggggcgggcgggcgggcgggatgccctgccctacgatgcctttg  
 tggctctcgacaaggcacagagcgcggtggccgactgggtgtacaacgagctgcgggtacggctagaggagcgcc  
 10 gtggacgagcagctccgctgtgctggaggaacgtgactgggtaccgggtaaaacgctctttgagaacctgt  
 gggcctcagtttacagcagccgcaagatgtgttctgtgctggccacacagacagggtcagcgccctcttgcg  
 ccagctttctgtggccagcagcgctgtggaggaccgcaaggacgtgtgtgtgctgtgatcctgctgccccg  
 acgcccacgctcccgctatgtgcggctgcgcccagcgcctctgcccagagcgtcctctctggccccaccagc  
 ccagtggccagcgcagcttctgggcccagctgggacggccctgaccagggaaccagcacttctataaccaga  
 15 acttctgccccggggccccacgacggcagagtgaccgcccagcaccccaagcctcctacaccttgctgtctgctg  
 ggatgcccggg

## SEQ ID NO:28 (Feline TLR9)

atgggcccctgccatggcgccctgcacccctgtctctcctgggtgcaggtgcgcgctggccgtggccctggcc  
 20 cagggcacctgctgctttctgcccctgtgagctccagcgccacggcctgggtgaattgcgactggctgttctc  
 aagtccgtgcccacttctcggcgagcgcccggtggtaacgtcaccagcctttccctgactccaaccgcatc  
 caccacctccagcactccgactttgtccacctgtccagcctgcggcgctctcaacctcaaaggcttccgccc  
 gccagcctcagccccatgcaacttccctgtcacatgaccattgagccccacaccttccctggccgtgcccacctg  
 gaggagctgaacctgagctacaacagcatcacgacagtaccgcccctgccagttccctcgtgtccctgtccttg  
 25 agccgtaccaacatcctggtgctggaccctgcaacctgcgagggctgcactccctgcgctttctgttccctggat  
 ggcaactgctactacaagaacccctgcccgcaggccctgcaggtggccccggggcgccctccttggcctgggcaac  
 cttaacgacctgtcactcaagtacaacaacctcactgcggtgccccgcggcctgccccccagcctggagtacctg  
 ctattgtcctaccacatcatcaccctggcactgaggacctggccaacctgaccgcccctgctgtgctcgat  
 gtgggtgggaactgcccgtcgtgtgaccacgcccgaacccctgtatggagtggcccaagggttcccgccacctg  
 30 caccctgacaccttcagccacctgaaccacctcgaaggcctgggtgtgaaggacagctctctctacaacctgaac  
 ccagatgggttccatgcccctgggcaacctcatggtgctggacctgagtgagaacttccctatatgactgcatcacc  
 aaaaccacagccttccaggccctggcccagctgcgcagactcaacttgtctttcaattaccacaagaagggtgctc  
 ttgcccacctgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatgcatggcatcttc  
 ttccgctcgtcagcgagaccagctccggtcgttggctccacctgcccctgctccagagtctgcacctgcagatg  
 35 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgtcagacaac  
 cgcataagtggagccatggagctggcggtgccacggggagggtggatgggtggggagagagtcgggctccgcatct  
 ggggacctagctctggggccaccgggacccctagctccgagggttcatgccaggctgcaagacctcaacttc  
 accttggacctgtcacggaacaacctagtgaacatccagccagagatgtttgcccggctctcgcgctccagtg  
 ctgctcctgagccgcaacagcatctcgcaggcagtcacaggctcacaatttatgcccgtgaccagcctgcagggtg  
 40 ctggacctgtcccataacaagctggacctgtaccatgggctctttcacaggagctgcccgggctggaggccctg  
 gacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagctttgtggcacagctgccc  
 gccctgcgctatctcagcctggcgacacacagccgtgtgtcccagcagctctgcagcgcctcgtg  
 cgggcttggacttcagcggcaatgccttgagccggatgtgggcccaggagacctgtatctccacttcttcga  
 ggctgaggagcctgggtccggttggatctgtcccagaatcgccctgcataacctcttgccacgcacctggacaac  
 45 ctccccagagcctgcggctgctgctctccgtgacaattatctggctttcttcaactggagcagcctgggtctc  
 ctccccaggtggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgctaatgga  
 accagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttgcctctggccacc  
 aggtgctgagagctcaacctcagtgccaacgcctcaagacgggtggagccctcctgggttcgggttctctagcggg  
 acctgaaagtcttagatgtgactggcaacccctgcaactgcgctgtggggcgccctcgtggacttcttgcgtg  
 50 gaggtgcaggctgcagtgcccggcctgcaggccctgcaagtgtggcagtcacaggtcagctccagggcgcgagc  
 atctttgcccaggtctgcgctctgctggatgaggccctcctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

#### SEQ ID NO:29 (Murine TLR9)

MVLRRRTLHPLSLLVQAQAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 15 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL  
 SHTNIIIVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTPGALLGLSNLTHLSLKYNNTLTKVPRQLPPSLEYL  
 LVSYNLIIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCI ECGQKSLHLHPETFHHLSHLEGLVLKDSLSLHTLN  
 SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF  
 20 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRISGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKL DLYHWKSFSELPQLQALDLSYNSQPFMSKGI GHNFSFVAHLSMLHLSLAHNDI HTRVSSHLSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKL DLSQNNLHILRPQNL DNLPKSLKLLSLRDNYLSFFNWTSL  
 25 FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVLDVRSNPLHCACGAAFVDLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLL  
 AVAVGMVVPILHHL CGWDVWYCFHLCLAWPL LARSRSQAQALPYDAFVVF DKAQSAVADWVYNELRVRL EERRG  
 RRALRLCLEDRDWLPGQTLFENLWASIYGRKTLFVLAHTDRVSGLLRTSFLLAQQRLL EDRKD VVVVLILRPDA  
 HRSRYVRLRQRLCRQSVLFWPQQPNGQGGFWAQLSTALTRDNRHFYNQNF CRGPTAE

#### SEQ ID NO:30 (Murine TLR9)

MVLRRRTLHPLSLLVQAQAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 30 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL  
 SHTNIIIVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTPGALLGLSNLTHLSLKYNNTLTKVPRQLPPSLEYL  
 LVSYNLIIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCI ECGQKSLHLHPETFHHLSHLEGLVLKDSLSLHTLN  
 SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF  
 35 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRISGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKL DLYHWKSFSELPQLQALDLSYNSQPFMSKGI GHNFSFVAHLSMLHLSLAHNDI HTRVSSHLSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKL DLSQNNLHILRPQNL DNLPKSLKLLSLRDNYLSFFNWTSL  
 40 FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVLDVRSNPLHCACGAAFVDLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

#### SEQ ID NO:31 (Murine TLR9)

tgctcagagggagcctcgggagaatcctccatctcccaacatgggtctccgtcgaaggactctgcaccccttgctc  
 ctccctggtacaggctgcagtgctggctgagactctggccctgggtacctgcctgccttccctaccctgtgagctg

- 25 -

aagcctcatggcctgggtgactgcaattggctgttccctgaagtctgtaccccgtttctctgcggcagcatcctgc  
tccaacatcacccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc  
aacctgcggcagctgaacctcaagtgggaactgtccaccactggccttagccccctgcacttctcttgccacatg  
accattgagcccagaaccttcttggtatgctgactggaggagctgaacctgagctataatgggtaccaccact  
5 gtgccccgactgccagctccctgggtgaatctgagcctgagccacaccaacatcctgggtctagatgctaacagc  
ctcgcccggtatatacagcctgcgcgttctcttcatggacgggaactgctactacaagaacctcctgcacaggagcg  
gtgaaggtgacccccaggcgccctcctgggcctgagcaatctcaccatctgtctctgaagtataacaacctcaca  
aaggtgccccgccaactgccccccagcctggagtacctcctgggtgtcctataacctcattgtcaagctggggcct  
gaagacctggccaatctgacctcccttcgagtacttgatgtgggtgggaattgcccgtcgctgcgacctgcccc  
10 aatccctgtatagaatgtggccaaaagtcctccactgcacctgagaccttccatcacctgagccatctggaa  
ggcctgggtgctgaaggacagctctctccatacactgaactcttccctgggttccaaggtctgtaaacctctcggtg  
ctggacctaaagcgagaacttctctatgaaagcatcaaccacaccaatgccttccagaacctaacccgcctgcgc  
aagctcaacctgtccttcaattaccgcaagaaggtatccttggccgcctccacctggcaagttccttcaagaac  
ctgggtgctactgcaggagctgaacatgaacggcatcttcttccgctcgctcaacaagtacacgctcagatggctg  
15 gccgatctgccccaaactccacactctgcatcttcaaatagaacttcatcaaccaggcacagctcagcatcttgggt  
accttccgagcccttcgcttgggtgacttgctcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc  
cctgaagaggcagatgatgcagagcaggagagctgtgtctcggtatcctcaccagctccactgagcaccct  
gcttctaaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctctcggtg  
atcaagccagagatgttgtcaatctctcacgcctccagtgctttagcctgagccacaactccattgcacaggct  
20 gtcaatggctctcagttcctgcgcgtgactaatctgcaggtgctggacctgtccataacaaactggacttgtac  
cactggaaatcggttcagtgcagctaccacagttgcagggcctggacctgagctacaacagccagccctttagcatg  
aagggtataggccacaatttcagtttgggtggccatctgtccatgctacacagccttagcctggcacacaatgac  
attcatacccggtgtgtcctcacatctcaacagcaactcagtgaggttcttgacttcagcggcaacgggtatgggc  
cgcatgtgggatgagggggccttctctccatttcttccaaggcctgagtgccctgtgaagctggacctgtct  
25 caaataaacctgcatactctccggccccagaaccttgacaacctccccagagcctgaagctgctgagcctccga  
gacaactacctatcttctttaaactggaccagtctgtccttccctgccccaaactggaagtcctagacctggcaggc  
aaccagctaaaggccctgaccaatggcaccctgcctaatggcaccctcctccagaaactggatgtcagcagcaac  
agtatcgctctctgtggtcccagccttcttcgctctggcggtcgagctgaaagaggtcaacctcagccacaacatt  
ctcaagacgggtggatcgctcctgggttggggccattgtgatgaacctgacagttctagacgtgagaagcaacct  
30 ctgactgtgctgtggggcagccttcgtagacttactgttggaggtgcagaccaaggtgcctggcctggctaact  
gggtgaagtgtggcagccccggccagctgcagggcctgagcatcttcgcacaggacctgcggctgtgctggat  
gaggtcctctcttgggactgcttggccttcaactctggctggtggcgtgggcatgggtgcttactgcaac  
catctctcgggctgggacgtctgggtactgttctcatctgtgctggcatggctaccttggctggcccgagccga  
cgagcgccccagctctccctatgatgccttcgtgggtgttcgataaggcacagagcgagtgctgggactgggtg  
35 tataacgagctgcgggtgcggctggaggagcggcgcggtcgccgagccctacgctgtgtctggaggaccgagat  
tggctgcctggccagacgtcttcgagaacctctgggttccatctatgggagccgcaagactctatttgtgctg  
gcccacaaggaccgcgtcagtgccctcctgcgcaccagcttctctgctggctcagcagcgccgtgttggaaagaccgc  
aaggacgtgggtgttgggtgatcctgctccggatgccaccgctcccgctatgtgagctgcgcagcgctctc  
tgccgcagaggtgtgctctctggccccagcagcccaaggcgaggggggttctgggcccagctgagtaacagcc  
40 ctgactagggacaaccgccacttctataaccagaacttctgcccggggacctacagcagaatagctcagagcaaca  
gctggaaacagctgcatcttcatgacctggttcccgagttgctctgcctgc

## SEQ ID NO:31 (Murine TLR9)

atggttctccgtcgaaggactctgcacccttgtccctcctggtagaggctgcagtgctggctgagactctggcc  
45 ctgggtaccctgcctgccttccctaccctgtgagctgaagcctcatggcctgggtgactgcaattggctgttccctg  
aagtctgtaccccgtttctctgcggcagcatcctgctccaacatcaaccgcctctccttgatctccaaccgtatc  
caccacctgcacaactccgacttcgtccacctgtccaacctgcggcagctgaacctcaagtggaaactgtccacc  
actggccttagccccctgcacttctcttgccacatgacctgagccagaaccttcttggtatgctgactg  
50 gaggagctgaacctgagctataatgggtatcaccactgtgcccgactgcccagctccttggtgaatctgagcctg  
agccacaccaacatcctgggtctagatgctaacagcctgcgcggcctatacagcctgcgcgttctcttgag  
gggaactgctactacaagaacctcctgcacaggagcgggtgaagtgacccaggcgccctcctgggctgagcaat  
ctcaccatctgtctctgaagtataacaacctcacaaggtgccccgccaactgccccccagcctggagtacctc  
ctggtgtcctataacctcattgtcaagctggggcctgaagacctggccaatctgacctcccttcgagtacttgat  
gtgggtgggaattgcccgtcgctgcgacctgcccccaatccctgtatagaatgtggccaaaagtcctccacctg  
55 caccctgagaccttccatcacctgagccatctggaaggcctgggtgctgaaggacagctctctccatacactgaac  
tcttctgggttcaaggtctgggtcaacctctcggtgctggacctaaagcgagaacttctctatgaaagcatcaac  
cacaccaatgccttccagaacctaacccgcctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc

- 26 -

tttgcccgcctccacctggcaagttccttcaagaacctggtgtcactgcaggagctgaacatgaacggcatcttc  
 ttcgctcgctcaacaagtacacgctcagatggctggcgatctgcccacctccacactctgcatcttcaaagt  
 aacttcatcaaccaggcacagctcagcatctttggtaccttccgagcccttcgctttgtggacttgtcagacaat  
 5 cgcacagtggtggccttcaacgctgtcagaagccaccctgaagaggcagatgatgcagagcaggaggagctgttg  
 tctgcggtacctcaccagctccactgagcaccctgtcttaagaacttcatggacaggtgtaagaacttcaag  
 ttaccatggacctgtctcggaacaacctggtgactatcaagccagagatgtttgtcaatctctcagcctccag  
 tgtcttagctgagccacaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaatctgcag  
 gtgctggacctgtcccataaacaactggacttgaccactggaaatcggtcagtgagctaccagattgcaggcc  
 10 ctggacctgagctacaacagccagcccttagcatgaagggtataggccacaatttcagttttgtggcccatctg  
 tccatgctacacagccttagcctggcacacaatgacattcatacccggtgtgtcctcacatctcaacagcaactca  
 gtgaggtttctgacttcagcggcaacggtatggcgcgatgtgggatgaggggggctttatctccattttcttc  
 caaggcctgagtggtgctgaagctggacctgtctcaaaataacctgcatactctccggccccagaaaccttgac  
 aacctccccagagcctgaagctgtgagcctccgagacaactacctatctttctttaactggaccagtctgtcc  
 15 ttcctgcccacctggaagtcttagacctggcaggcaaccagctaaaggccctgaccaatggcacctgtccta  
 ggcacctctctccagaaactggatgtcagcagcaacagtatcgctctctgtggtcccagccttcttcgctctggcg  
 gtcgagctgaagaggtcaacctcagccacaacattctcaagacggtggatcgctcctggtttggcccatctg  
 atgaacctgacagttctagacgtgagaagcaacctctgcactgtgcctgtggggcagcctctcgtagacttactg  
 ttggaggtgcagaccaaggtgctggcctggctaattggtgtgaagtgtggcagccccggccagctgcagggcggt  
 20 agcatcttcgcacaggacctgcggtgtgcctggatgaggtcctctcttgggactgctttggc

## SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPALPCELQPHGLVNCNWFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 25 SHTNILMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTLVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNPCMECPRHFPQLHPDTFSLSLRLEGLVLKSSLSWLN  
 ASWFRGLNLRVLDLSENFLYKCTTKTKAFQGLTQLRKLNLNFYQKRVSFALHSLAPSGSLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVLQ  
 GDLAPAPVDTFSSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 30 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFQMVGHNFSFVAHLRTLRLHSLAHNNIHSQVSQQLCSTSL  
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRLLHTLLPQTLRNLPKSLQVLRRLRDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLNLSANALKTVDHWSFGPLAS  
 ALQILDVSNPLHCACGAAFMDLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLA  
 VALGLGVPMHLHLCGWDLYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKTQSAVADWVYNELRGQLEECRG  
 35 RWALRLCLEERDWPGLKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLIEDRKDVVVLVILSPDG  
 RRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGMALTRDNHFFYNRNFQCGPTAE

## SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPALPCELQPHGLVNCNWFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 40 SHTNILMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTLVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNPCMECPRHFPQLHPDTFSLSLRLEGLVLKSSLSWLN  
 ASWFRGLNLRVLDLSENFLYKCTTKTKAFQGLTQLRKLNLNFYQKRVSFALHSLAPSGSLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVLQ  
 GDLAPAPVDTFSSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 45 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFQMVGHNFSFVAHLRTLRLHSLAHNNIHSQVSQQLCSTSL  
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRLLHTLLPQTLRNLPKSLQVLRRLRDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLNLSANALKTVDHWSFGPLAS  
 ALQILDVSNPLHCACGAAFMDLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFA

## 50 SEQ ID NO:35 (Human TLR9)

aggctgggtataaaaaatcttacttctctattctctgagccgctgctgcccctgtgggaagggacctcgagtgtga  
 agcatccttccctgtagctgctgtccagctgctgcccgcagaccctctggagaagcccctgccccccagcatgggt  
 tctgcccgcagcgcctgacccgctgtctctcctggtgcaggccatcatgctggccatgacctggcctgggt

- 27 -

accttgccctgccttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctgaagtct  
 gtgccccacttctccatggcagcaccctggtgcaatgtcaccagccttccctgtcctccaaccgcacccaccac  
 ctccatgattctgactttgcccacctgcccagcctgcccagctctcaacctcaagtggaaactgcccgcgggttggc  
 ctacgccccatgcacttccccctgccacatgaccatcgagcccagcacttcttggctgtgcccaccctggaagag  
 5 ctaaactgagctacaacaacatcatgactgtgcctgcgctgcccacaaatccctcatatccctgtccctcagccat  
 accaacatcctgatgctagactctgccagcctgcgcggcctgcatgccctgcgcttccctattcatggacggcaac  
 tgttattacaagaaccctgcaggcaggcactggaggtggccccgggtgccctccttggcctgggcaacctcacc  
 cactgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctgctgttg  
 tctacaaccgcacgtcaaaactggcgccctgaggacctggccaatctgacccgcctgcgtgtgctcgatgtgggc  
 10 ggaaattgcccgcctgcgaccacgctcccaacccctgcatggagtgcctcctgcacttccccagctacatccc  
 gatccttcagccacctgagccgtcttgaaggcctggtgttgaggacagttctctctcctggtggaatgccagt  
 tgggtccgtgggctgggaaacctccgagtgctggacctgagtgagaacttccctctacaaatgcatcactaaaacc  
 aaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaagagggtgtcctttgcc  
 cactgtctctggcccccttccctcgggagcctggtgcgcctgaaggagctggacatgcacggcatcttcttccgc  
 15 tactcgatgagaccacgctccggccactggccgcctgcccacgtccagactctgcgtctgcagatgaacttc  
 atcaaccaggcccagctcggcatcttcaggcccttccctggcctgcgctacgtggacctgtcggacaaccgcac  
 agcggagcttcggagctgacagccaccatgggggagggagatggaggggagaaggctcgtgctgcagcctggggac  
 ctgtctccggccacctggacactccagctctgaagacttcaggcccaactgcagcacctcaacttcaccttg  
 gatctgtcacggaacaacctgggtgacctgacgcggagatgtttgccagctctcgcacctgcagtgccctgcgc  
 20 ctgagccacaactgcatctcgcaggcagtcattggctcccagttccctgcgcgtgacccgtctgcaggtgctagac  
 ctgtcccgcaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctggacctc  
 agctacaacagccagcccttggcatgcaggcgctggggccacaacttcagcttctggtgctcactgcgcacctg  
 cgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctgcggggcc  
 ctggacttcagcggcaatgcactgggcatatgtgggcccagggagacctctatctgcacttcttccaaggcctg  
 25 agcggtttgatctggctggacttgcctccagaacgcgctgcacacctcctgccccaaacctgcgcaacctcccc  
 aagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtggtggagcctccacttccctgcc  
 aaactggaagtctctgacctggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggcaccgg  
 ctccggaggctggatgtcagctgcaacagcatcagcttctggtggccccggcttcttttccaaggccaaggagctg  
 cgagagctcaaccttagcgccaacgcctcaagacagtgaggacctcctgggttggggccctggcgagtgccctg  
 30 caaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttatggacttccctgctggaggtg  
 caggctgcgcgtgcccggctctgcccagccgggtgaagtgtggcagtcggggccagctccaggccctcagcatcttt  
 gcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttgcgcctctcgtgctggctgtggct  
 ctgggctgggtgtgcccctgctgcatcacctctgtggctgggacctctgggtactgcttccacctgtgcctggcc  
 tggcttccctggcgggggcggaagtggcgagatgaggatgcctgcccctacgatgccttctggtgctctcgac  
 35 aaaaagcagagcgagtgaggagctgggtgtacaacgagcttccggggcagctggaggagtgccgtgggctggtg  
 gactccgcctgtgcctggaggaaacgcgactggctgcctggcaaaacctctttgagaacctgtgggctcgtgct  
 tatggcagccgcaagacgctgtttgtgctggccacacggaccgggtcagtggtctcttgcgcgccagcttccctg  
 ctggcccagcagcgcctgtcggaggaccgcaaggacgctcgtggtgctggtgatcctgagccctcagggccgcgc  
 tccgctacgtgcggctgcgcagcgcctctgcgcagagtgctcctcctggtggcccacagccagctgggtcag  
 40 cgagctctctgggcccagctgggcatggcctgaccagggaacaaccaccttctataaccggaactctgcccag  
 ggacccacggcgaatagccgtgagccggaatcctgcacgggtgccacctccacactcacctcacctctgctgcc  
 tggctgacctccctgctgcctccctcacccacacctgacacagagca

## SEQ ID NO:36 (Human TLR9)

45 atgggtttctgcccagcgcctgacccgctgtctctcctggtgcaggccatcatgctggccatgacctggcc  
 ctgggtaccttgccctgccttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctg  
 aagtctgtgccccacttctccatggcagcaccctggtgcaatgtcaccagccttccctgtcctccaaccgcac  
 caccacctccatgattctgactttgcccacctgcccagcctgcccagctctcaacctcaagtggaaactgcccgcg  
 gttggcctcagcccccagcttccccctgccacatgaccatcgagcccagcacttcttggctgtgcccacctg  
 50 gaagagctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccacaaatccctcatatccctgtccctc  
 agccataccaacatcctgatgctagactctgccagcctgcgcggcctgcatgccctgcgcttccctattcatggac  
 ggcaactgttattacaagaaccctgcaggcaggcactggaggtggccccgggtgccctccttggcctgggcaac  
 ctaccacacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctg  
 ctgttgcctacaaccgcacgtcaaaactggcgccctgaggacctggccaatctgacccgcctgcgtgtgctcgat  
 55 gtggggcggaattgcccgcctgcgaccacgctcccaacccctgcatggagtgcctcctgcacttccccagcta  
 catcccgataccttcagccacctgagccgtcttgaaggcctggtgttgaggacagttctctctcctggtggaat  
 ccagattgggtccgtgggctgggaaacctccgagtgctggacctgagtgagaacttccctctacaaatgcatcact

- 28 -

aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaagaggggtgtcc  
 tttgccacctgtctctggcccttctcctcgaggagcctggcgccctgaaggagctggacatgcacggcatcttc  
 ttccgctcactcgatgagaccagctccggccactggcccgctgccatgctccagactctgcgtctgcagatg  
 aacttcatcaaccaggccagctcggcatcttcagggccttccctggcctgcgtacgtggacctgtcggacaac  
 5 cgcatcagcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcct  
 ggggaccttgctccggcccccagtggaactcccagctctgaagacttcaggcccaactgcagcacctcaacttc  
 accttggatctgtcacggaacaacctgggtgacctgcagccggagatgtttgccagctctcgcacctgcagtgc  
 ctgcgctgagccacaactgcatctcgcaggcagtcagtggctcccagttcctgcccgtgacctgtgcagggtg  
 cttagacctgtcccgcaataagctggacctctaccagagcactcattcacggagctaccgcgactggaggccctg  
 10 gacctcagctacaacagccagccctttggcatgcaggggcgtgggcccacaacttcagcttcgtggctcacctgcgc  
 accttgcgccacctcagcctggcccaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctg  
 cgggcccctggacttcagcggcaatgcactgggcccataatgtgggcccagggagacctctatctgcacttcttccaa  
 ggcttgagcgggttgatctggctggacttgctccagaaccgcctgcacacctcctgccccaaacctgcgcaac  
 ctccccaaagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtgggtggagcctccacttc  
 15 ctgccccaaactggaagtccctgcacctggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggc  
 acccggtccggaggtggatgtcagctgcaacagcatcagcttcgtggccccggcttcttttccaaaggccaag  
 gagctgcgagagctcaaccttagcgccaacgcctcaagacagtggaacctcctgggttgggcccctggcgagt  
 gccctgcaaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttaggacttctctgctg  
 20 gaggtgcagggtgcccgtgcccggctgcccagccgggtgaagtgtggcagtcggggccagctccagggcctcagc  
 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9  
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and  
 nucleic acid molecules encoding them are provided by the invention. The chimeric  
 25 polypeptides include at least one amino acid substitution based on a comparison of  
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,  
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple  
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in  
 Figure 1, can be used to identify and select individual amino acid positions and even  
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or  
 substitutions can be effected using methods known to those of ordinary skill in molecular  
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be  
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino  
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second  
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to  
 alter conformation. For example, conservative amino acid substitutions generally may be  
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),  
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-  
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide  
5 sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is  
10 operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase,  $\beta$ -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in  
15 eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.  
20 The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

25 In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid  
30 coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA



- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine  
10 dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15 
$$5'-N_1X_1CGX_2N_2-3'$$

wherein  $X_1$  and  $X_2$  are nucleotides, N is any nucleotide, and  $N_1$  and  $N_2$  are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments  $X_1$  is adenine, guanine, or thymine and/or  $X_2$  is cytosine, adenine, or thymine. In other embodiments  $X_1$  is cytosine and/or  $X_2$  is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a  
25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising  
30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the  $\beta$ -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease).

Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has  
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.  
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by  
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,  
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid  
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty  
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene  
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180  
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)  
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and  
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

	MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
	hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
	mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSLEP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test  
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of  
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory  
25 nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a  
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact  
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a  
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to  
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving  
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including  $\kappa$ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- $\kappa$ B. Examples of such promoters include, without limitation, those for NF- $\kappa$ B, IL-1 $\beta$ , IL-6, IL-8, IL-12 p40, CD80,  
25 CD86, and TNF- $\alpha$ . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase,  $\beta$ -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- $\alpha$ ). In  
30 certain embodiments the reporter is selected from IL-8, TNF- $\alpha$ , NF- $\kappa$ B-luciferase (NF- $\kappa$ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

*Mol Cell Biol* 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- $\kappa$ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF,  $\text{I}\kappa\text{B}$ , NF- $\kappa\text{B}$ , or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test



- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

### Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

*Cells and Tissues.* Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasy<sup>TM</sup> (Ambion<sup>®</sup>, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

*First-strand cDNA synthesis.* Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using  
5 SUPERScript™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T<sub>(18)</sub>]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at  
10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl<sub>2</sub>) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERScript™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:  
20 forward primer 5'-ACCTTGCCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix  
25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

*Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min  
30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZEROTM - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

*Results.* Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

#### Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, [www.cmbi.kun.nl/bioinf/tools/clustalw.shtml](http://www.cmbi.kun.nl/bioinf/tools/clustalw.shtml)). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in **Figure 1**. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

**Figure 2** presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

### Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- $\kappa$ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- $\kappa$ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- $\kappa$ B-luciferase reporter plasmid (NF- $\kappa$ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 $\mu$ M, TCGTCGTTTGTGCGTTTGTGCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 $\mu$ M, TGCTGCTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- $\kappa$ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 $\mu$ M; TCCATGACGTTTCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 $\mu$ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- $\kappa$ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates ( $2 \times 10^6$  cells/plate) with 16  $\mu$ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- $\kappa$ B-luciferase activity after stimulation with  
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20  $3 \times 10^6$  293T cells were electroporated with 5  $\mu$ g NF- $\kappa$ B-luc plasmid and 5  $\mu$ g of either horse TLR9-pcDNA3.1 plasmid or human TLR9-pcDNA3.1 plasmid at 200V, 975  $\mu$ F. After the electroporation the cells were plated in 96-well cell culture plates at  $2.5 \times 10^4$  cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and  
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in **Figure 3**.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982  
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

### Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

**Claims**

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

5

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

10

4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

15

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

20

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:  
aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;  
generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

25  
30



- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with  
5 the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a  
15 CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the  
20 initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred  
30 CpG DNA).

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5           12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10           14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:  
15           contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;  
              measuring a signal in response to the contacting; and  
              identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20           17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25           18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30           20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GCGGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, 5 GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the 10 contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

15 23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCCTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

Figure 1  
(1/3)

```

feline      MGPCHGALHPLSLLVQAAALAVALAQGTLPAPFLPCELPQRHGLVNCDWLFLKSVPHFSAAA 60
canine      MGPCRGALHPLSLLVQAAALALALAQGTLPAPFLPCELPQPHGLVNCNWFLKSVPRFSAAA 60
bovine      MGP-YCAPHPLSLLVQAAALAAALAEGLTPAPFLPCELPQPHGQVDCNWLFLKSVPHFSAGA 59
mouse       MGP-YCAPHPLSLLVQAAALAAALAEGLTPAPFLPCELPQPHGQVDCNWLFLKSVPHFSAGA 59
ovine       MGP-YCAPHPLSLLVQAAALAAALAEGLTPAPFLPCELPQPHGQVDCNWLFLKSVPRFSAGA 59
porcine     MGP-RCTLHPLSLLVQVTLAAALAAQGRLPAPFLPCELPQPHGLVNCNWFLKSVPHFSAAA 59
horse       MGPCHGALQPLSLLVQAAMLAVALAQGTLPAPFLPCELPQPHGLVNCNWFLKSVPHFSAAA 60
human       MGFCRSALHPLSLLVQAIMLAMTLALGTLPAPFLPCELPQPHGLVNCNWFLKSVPHFSMAA 60
rat         MVLCRRTLHPLSLLVQAIVLAEALALGTLPAPFLPCELPKPHGLVDCNWLFLKSVPHFSAAE 60
*           :*****. ** :* * *.*****: ;* *.:*****:*.

feline      PRGNVTSLSLSYNSRIHHLHDSDFVHLSLRLNLKWNCPASLSPMHFPCMTIEPHTFL 120
canine      PRGNVTSLSLSYNSRIHHLHDYDFVHFVHLRLNLKWNCPASLSPMHFPCMTIEPNTFL 120
bovine      PRANVTSLSLSISNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFL 119
mouse       PRANVTSLSLSISNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFL 119
ovine       PRANVTSLSLSISNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFL 119
porcine     PRANVTSLSLSNRIHHLHDSDFVHLSLRTNLKWNCPAGLSPMHFPCMTIEPNTFL 119
horse       PRDNVTSLSLSNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCMTIEPNTFL 120
human       PRGNVTSLSLSNRIHHLHDSDFVHLSLRLNLKWNCPVGLSPMHFPCMTIEPSTFL 120
rat         PRSNITSLSLIANRIHHLHDLDFVHLPNVRQLNLKWNCPVGLSPMHFPCMTIEPKTFL 120
*           *:*****:*****: **.: : *****.***:*.***** **

feline      AVPTLEELNLSYNSITTVPALPSSLVSLSLRTNIVLDPANLAGLSLRFLLDGNCCY 180
canine      AVPTLEDNLSYNSITTVPALPSSLVSLSLRTNIVLDPATLAGLYALRFLFLDGNCCY 180
bovine      AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCCY 179
mouse       AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCCY 179
ovine       AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCCY 179
porcine     AVPTLEELNLSYNSITTVPALPSSLVSLSLRTNIVLDPHTLGLHALRFLYMDGNCCY 179
horse       AVPTLEELNLSYNGITTVPALPSSLVSLSLRTNIVLQDPTSLTGLHALRFLYMDGNCCY 180
human       AVPTLEELNLSYNNIMTVPALPKSLISLSLSTNIMLDSASLAGLHSLRFLYMDGNCCY 180
rat         AMRMLEELNLSYNGITTVPRLPSSLTNLSLSTNIVLDDASSLAGLSLRLVFLYMDGNCCY 180
*           *:*****.* *** **.* * **:*.* *.: :*:***:*.*****

feline      KNPCQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYLLSYNHIITLAPEDL 240
canine      KNPCQALQVAPGALLGLGNLTHLSLKYNNTVPRGLPPSLEYLLSYNHIITLAPEDL 240
bovine      MNPCPRALEVAPGALLGLGNLTHLSLKYNNTVPRGLPPSLDTLLSYNHIVTLAPEDL 239
mouse       MNPCPRALEVAPGALLGLGNLTHLSLKYNNTVPRGLPPSLDTLLSYNHIVTLAPEDL 239
ovine       KNPCQALEVAPGALLGLGNLTHLSLKYNNTVPRGLPPSLDTLLSYNHIITLAPEDL 239
porcine     KNPCQALEVVPGALLGLGNLTHLSLKYNNTVPRSLPPSLETLLSYNHIVTLTPEDL 239
horse       KNPCGRALEVAPGALLGLGNLTHLSLKYNNTVPRSLPPSLEYLLSYNHIIVTLAPEDL 240
human       KNPCQALEVAPGALLGLGNLTHLSLKYNNTVPRNLPPSLEYLLSYNRIIVKLAPEDL 240
rat         KNPCNGAVNVTDPAPFLGLSNLTHLSLKYNNTVPRQLPPSLEYLLSYNLVKGAEEDL 240
*           *** *:*.*.***** ***** ** *:*****:*.***

feline      ANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLPDTFSLHNLHLEGLVLKDSSLYNLN 300
canine      ANLTALRVLDVGGNCRRCDHARNPCRECPKGFQPLHPNTFGHLSHLEGLVLKDSSLYSLD 300
bovine      ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSLHSLRLEGLVLKDSSLYKLE 299
mouse       ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSLHSLRLEGLVLKDSSLYKLE 299
ovine       ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSLHSLRLEGLVLKDSSLYKLE 299
porcine     ANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSLHSLRLEGLVLKDSSLYQLN 300
horse       ANLTALRVLDVGGNCRRCDHARNPCRECPKHFQPLHSDTFSLHSLRLEGLVLKDSSLYQLN 300
human       ANLTALRVLDVGGNCRRCDHARNPCMECPRHFPQLHPDTFSLHSLRLEGLVLKDSSLSWLN 300
rat         ANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHLSHLEGLVLKDSSLSHSLN 300
*           *****:*****:*****: * * *: *.:** *.:*****:**** *:

feline      PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRLNLNLSFNHYHKKVSFAHLHLAPSF 360
canine      PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRLNLNLSFNHYHKKVSFAHLHLASSF 360
bovine      KDWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRLNLNLSFNHYHKKVSFAHLHLASSF 359
mouse       KDWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRLNLNLSFNHYHKKVSFAHLHLASSF 359
ovine       KDWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLRLNLNLSFNHYHKKVSFAHLQLAPSF 359
porcine     TRWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRLNLNLSFNHYHKKVSFAHLHLAPSF 359
horse       PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRLNLNLSFNHYHKKVSFAHLTLAPSF 360
human       ASWFRGLGNLTVLDLSENFLYKICITKTKAFQGLTQLRLNLNLSFNHYQKRVSAHLHLAPSF 360
rat         SKWFQGLANLSVLDLSENFLYKINIKTSFQNLTRLRLNLSFNHYCKKVSFAHLHLASSF 360
*           **:*. * *****. *.*. * .:*** *:*****:*****:*.***

```

**Figure 1**  
**(2/3)**

```

feline      GSLLSLQQLDMHGIFFRSLSETTLRSVLHLPMLQSLHLQMNFINQAQLSIFGAFPLGRYV 420
canine      GSLLSLQELDIHGIFFRSLSKTTQLSLAHLPMQLRLHLQLNFIQAQLSIFGAFPLGRYV 420
bovine      GSIVSLEKLDMHGIFFRSLTNITLQSLTRLPKQLSLHLQLNFINQAQLSIFGAFPSLLFV 419
mouse       GSIVSLEKLDMHGIFFRSLTNITLQSLTRLPKQLSLHLQLNFINQAQLSIFGAFPSLLFV 419
ovine       GGLVSLEKLDMHGIFFRSLTNITLRLPTQLPKQLSLQLNFINQAELSIFGAFPSLLFV 419
porcine     GHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPLGLLYV 419
horse       GSLLSLQELDMHGIFFRSLSQKTLQPLARLPMQLRLYLQMNFINQAQLGIFKDFPLGRYI 420
human       GSLVALKELDMHGIFFRSLDETTLRLPLARLPMQLTLRLQMNFINQAQLGIFRAFPGLRYV 420
rat         KSLVSLQELNMNGIFFRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFV 420
           * :*:*:*:*:*: * : **: * . ** *: * **:*:*.**:*:* * . * : :

feline      DLSDNRISGAMELAAATGEVDG--GERVRLPSGDLALGPPGTPSSEGFMPCCKTLNFTLD 478
canine      DLSDNRISGAAPAAATGEVADCGERVWPQSRDLALGLTGPSEAFMPSCRTLNFTLD 480
bovine      DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
mouse       DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
ovine       DLSDNRISGAARPVAALGEVDS--GVEVWRWPRGLAPGPLAAVSAKDFMPSCN-LNFTLD 476
porcine     DLSDNRISGAARPVAITREVDG--REVRVWLPNRNLPAPRLDTRSEDFMPNCKAFSFTLD 477
horse       DLSDNRISGAVEPVATTGEVDG--GKKVWLTSRDLTPGPLDTPSSEDFMPSCNLSFTLD 478
human       DLSDNRISGASELTATMGEADG--GEKVWLQPGDLAPAPVDTPSSEDFRPNCSFTLNFTLD 478
rat         DLSNNRISGPPTLSRVAPEKAD-EAEKGVWPASLTLPALPSTPVSKNFMVRCKNLRFMTD 479
           ***:*****. * . . .*: : : * * : **:*

feline      LSRNNLVTTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPPLTSLOVLDLSHNKLDLYHG 538
canine      LSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNLRVLDLSHNKLDLYHG 540
bovine      LSRNNLVTTIQPEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSRVLDSHNKLDLYHG 536
mouse       LSRNNLVTTIQPEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSRVLDSHNKLDLYHG 536
ovine       LSRNNLVTTIQPEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSRVLDSYNKLDLYHG 536
porcine     LSRNNLVTTIQSEMFARLSRLQCLRLSHNSISQAVNGSQFVPLTSRVLDSHNKLDLYHG 537
horse       LSRNNLVTVQPEMFAQLSRDLQCLRLSHNSISQAVNGSQFVPLTSLOVLDLSHNKLDLYHG 538
human       LSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHE 538
rat         LSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLKVLDLSYNKLDLYHS 539
           ***** :*: * :*:*.** *:*.**:*:*****:*: * :*****:*****

feline      RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSSQQLCSA 598
canine      RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNGIHSRVSSQQLRSA 600
bovine      RSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSSQKLSSA 596
mouse       RSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSSQKLSSA 596
ovine       RSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSSQKLSSA 596
porcine     RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSSQQLCSA 597
horse       RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPTRLRYLSLAHNGIHSRVSSQQLCST 598
human       HSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAHLRTRLRLSLAHNNIHSQVSSQQLCST 598
rat         KSFSLEPQLQALDLSYNSQPFMSQGIHNFSLANLSRLQNLSLAHNDIHSRVSSRLYST 599
           :*:***:*:***** **:***:*:* * : *****.**:*. * :

feline      SLRALDFSGNALSQMWAEGLDLYLHFFRGLRSLVRLDLSQNLHTLLPRTLNDLNPKSRLRL 658
canine      SLRALDFSGNTLSQMWAEGLDLYLRFFQGLRSLVQLDLSQNLHTLLPRNLNDLNPKSRLRL 660
bovine      SLRALDFSGNLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNDLNPKSRLRL 656
mouse       SLRALDFSGNLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNDLNPKSRLRL 656
ovine       SLRALDFSGNLSQMWAEGLDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNDLNPKSRLRL 656
porcine     SLRALDFSGNDLSRMWAEGLDLYLRFFQGLRSLVWLDLSQNLHTLLPRALNDLNPKSRLKHL 657
horse       SLWALDFSGNLSQMWAEGLDLYLRFFQGLRSLIRLDLSQNLHTLLPCTLGNLNPKSRLQLL 658
human       SLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSQNLHTLLPQTLRNLNPKSRLQVL 658
rat         SVEYLDPSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSQNLKHLIRPQNLNLYLPKSRLTKL 659
           *: ***** :*: * * ***** **: * .*: *****:*: * * * ***** *

feline      RLRDNYLAFFNWSSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 718
canine      RLRDNYLAFFNWSSSLALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSIGFVVP 720
bovine      RLRDNNLAFFNWSSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP 716
mouse       RLRDNNLAFFNWSSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP 716
ovine       RLRDNNLAFFNWSSSLTVLQLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVTP 716
porcine     HLRDNNLAFFNWSSSLTLLPKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSNSIGFVNP 717
horse       RLRNNYLAFFNWSSSLTLLPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVP 718
human       RLRDNYLAFFKWWSLHFLPKLEALDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAP 718
rat         SFRDNHLSFFNWSSSLAFLPNRLDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIGFVVP 719
           :*: * :*: * * * .**.* ***** **: * * :*: * * * * * .

```

feline	SFFALATRLRELNLNSANALKTVEPSWFGSLAGTLKVLVDVTGNPLHCACGAAFVDFLLEVQ	778
canine	SFFALAVRLRELNLNSANALKTVEPSWFGSLAGALKVLVDVTANPLHCACGATFVDFLLEVQ	780
bovine	GGFVVRATRLRIELNLNSANALKTVDPSPWFGSLAGTLKILDVSNAPLHCACGAAFVDFLLERQ	776
mouse	GGFVVRATRLRIELNLNSANALKTVDPSPWFGSLAGTLKILDVSNAPLHCACGAAFVDFLLERQ	776
ovine	GGFVLANRLKELNLNSANALKTVDPFWFGRLTETLNILDVSNAPLHCACGAAFVDFLLEMQ	776
porcine	GGFALAKQLEELNLNSANALKTVEPSWFGSMVGNLKVLDVSNAPLHCACGATFVGFLLEVQ	777
horse	GGFALATRLRELNLNSANALRTEEPSWFGFLAGSLEVLVDVSNAPLHCACGAAFVDFLLQVQ	778
human	GGFSKAKELRELNLSANALRTEEPSWFGFLASALQILDVSNAPLHCACGAAFVDFLLEVQ	778
rat	AFALAVELKEVNLNSHNLTKTVDSWFGPIVMNLTVDVSSNPLHCACGAFFVDLLLEVQ	779
	..** * . * :*** * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
feline	AAVPGPLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFGLSLLTVALGLAVPMLHHI	838
canine	AAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFGLSLLAVALSLAVPMLHQI	840
bovine	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGGLSLLMVALGLAVPMLHHI	836
mouse	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGGLSLLMVALGLAVPMLHHI	836
ovine	AAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSLDCFGGLSLLMVALGLAVPMLHHI	836
porcine	AAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDETLSWNCCFGLSLLAMALGLVVPMLHHI	837
horse	AAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGGLSLLVVALGLAMPMLHHI	838
human	AAVPGPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFGLSLLAVALGLVGPMLHHI	838
rat	TKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGGLSLLAVAVGTVLPLLQHI	839
	****. * .**** * * * :*****. ** ** :*** :* : . :* :* : *	
feline	CGWDLWYCFHLCLAWLPRRGR--RGADALPYDAFVVDKAQSAVADWVYNELRVLEER	896
canine	CGWDLWYCFHLCLAWLPRRGR--RGVDALAYDAFVVDKAQSSVADWVYNELRVQLEER	898
bovine	CGWDLWYCFHLCLAWLPRRRQ--RGEDTLLYDAVVVDKQVSAVADWVYNELRVQLEER	894
mouse	CGWDLWYCFHLCLAWLPRRRQ--RGEDTLLYDAVVVDKQVSAVADWVYNELRVQLEER	894
ovine	CGWDLWYCFHLCLAWLPRRRQ--RGEDTLLYDAFVVDKAQSAVADWVYNELRVQLEER	894
porcine	CGWDLWYCFHLCLAWLPHRGQR--RGADALFYDAFVVDKAQSAVADWVYNELRVQLEER	895
horse	CGWDLWYCFHLGLAWLPRRGWQ--RGADALSYDAFVVDKAQSAVADWVYNELRVLEER	896
human	CGWDLWYCFHLCLAWLPRRGWQ--RGADALSYDAFVVDKAQSAVADWVYNELRVLEER	896
rat	CGWDLWYCFHLCLAWLPLLRGR--RSAQALPYDAFVVDKQVSAVADWVYNELRVLEER	898
	****.***** ** ** * . :* ****.*****.***:*****:*****:*****:*****	
feline	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQR	956
canine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQR	958
bovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMTFVLDHTDRVSGLLRASFLLAQQR	954
mouse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMTFVLDHTDRVSGLLRASFLLAQQR	954
ovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMTFVLDHTDRVSGLLRASFLLAQQR	954
porcine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMTFVLAHTDRVSGLLRASFLLAQQR	955
horse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQR	956
human	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMTFVLAHTDQVSGLLRASFLLAQQR	956
rat	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMTFVLAHTDQVSGLLRASFLLAQQR	958
	*** *****:***:***:*****:*.*** :*** :*:*****:*****:*****	
feline	LEDKRDVVVLVILRPAHRSRYVRLRQLCRQSVLLWPHQPSGQSFQAQLGTALTRDNQ	1016
canine	LEDKRDVVVLVILRPAHRSRYVRLRQLCRQSVLLWPHQPSGQSFQAQLGTALTRDNR	1018
bovine	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQANLGTALTRDNR	1014
mouse	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQANLGTALTRDNR	1014
ovine	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQANLGTALTRDNR	1014
porcine	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQAQLGTALTRDNH	1015
horse	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQAQLGTALTRDNH	1016
human	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQAQLGTALTRDNH	1018
rat	LEDKRDVVVLVILRPAAYRSRYVRLRQLCRQSVLLWPHQPSGQSFQAQLGTALTRDNH	1018
	***** * . *****:***** ** ****:*. *****:	
feline	HFYNNFCRGPTTAE-----	1031
canine	HFYNNFCRGPTTAE-----	1032
bovine	HFYNNFCRGPTTAE-----	1029
mouse	HFYNNFCRGPTTAE-----	1032
ovine	HFYNNFCRGPTTAE-----	1029
porcine	HFYNNFCRGPTTAE-----	1030
horse	HFYNNFCRGPTTAE-----	1031
human	HFYNNFCRGPTTAE-----	1032
rat	HFYNNFCRGPTTAE-----	1032
	*****.*****	

Figure 2

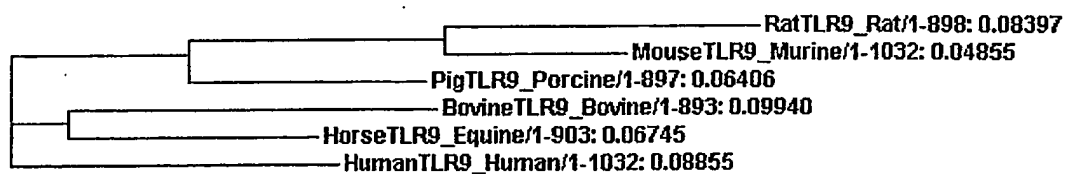
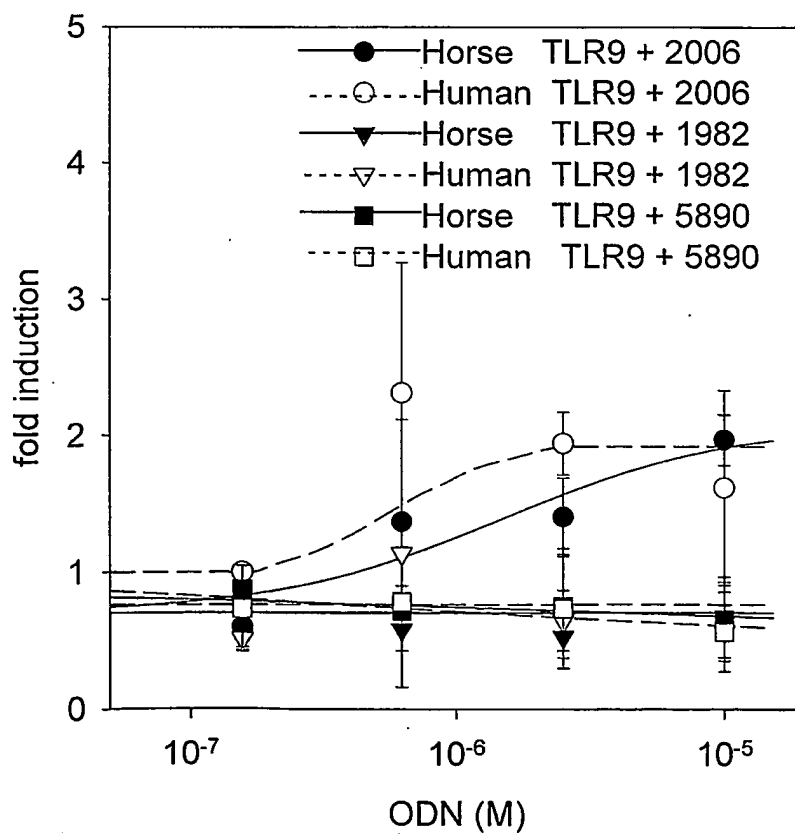


Figure 3



## SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH  
University of Saskatchewan  
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040W000

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
130 135 140



Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610	615	620
Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys		
625	630	635 640
Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu		
	645	650 655
Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser		
	660	665 670
Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn		
	675	680 685
Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu		
	690	695 700
Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala		
705	710	715 720
Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn		
	725	730 735
Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn		
	740	745 750
Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly		
	755	760 765
Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly		
	770	775 780
Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg		
785	790	795 800
Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser		
	805	810 815
Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val		
	820	825 830
Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe		
	835	840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser  
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser  
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 2  
 <211> 821  
 <212> PRT  
 <213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
 50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
 100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe  
 610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu  
 645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser  
 660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn  
 675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala  
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

	725		730		735
Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn					
	740		745		750
Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly					
	755		760		765
Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly					
	770		775		780
Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg					
	785		790		795
					800
Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser					
	805		810		815
Arg Asp Cys Phe Gly					
	820				

<210> 3  
 <211> 3099  
 <212> DNA  
 <213> Rattus norvegicus

<400> 3  
 atggtttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagagc cgcagtgtg 60  
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120  
 ggcttggttag actgcaactg gctcttcctg aagtctgtgc ctactttctc tgccgcagaa 180  
 ccccggttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctogactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctcctgc cgcattacca ttgagcccaa aaccttcctg 360  
 gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcaacggggc ggtgaacctg acccggagc ccttctggtg cttgagcaac 600  
 ctacccactc tgtcccttaa gtataacaac ctacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtcctataac ctcatcgta agctgggggc cgaagaccta 720  
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgcccgtc ctgtgatcac 780



gcccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc	840
catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctcgctgaac	900
tccaagtggg tccaggggtct ggcgaacctc tcggtgctgg acctaaagcga gaactttctc	960
tacgagagca tcaacaaaaac cagcgccctt cagaacctga cccgtctgcg caagctcgac	1020
ctgtccttca attactgcaa gaaggatatc ttcgcccgc tccacctggc aagttccttc	1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac	1140
aagaacacgc tcaggtgggt ggctgggtct cccaagctcc acacgctgca ccttcaaatg	1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg	1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag	1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccgagc tctcccgagc	1380
actcccgctc caaagaactt catggctcagg tgtaagaacc tcagattcac catggacctg	1440
tctcggaaca accagggtgac tatcaagcca gagatgttgc tcaacctctc ccatctccag	1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg	1560
ctgaccaacc tgaagggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa	1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc	1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac	1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca	1800
gtggagtatc tggacttcag cggcaacggg gtgggcccga tgtgggacga ggaggacctt	1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag	1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt	1980
ttcogtgaca atcacctctc tttctttaac tggagcagtc tggccttctc gcccaatctg	2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaata	2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc	2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact	2220
gtggatcgct cctgggtttg gccattgtg atgaacctga cggttctaga cgtgagcagc	2280
aaccctctgc attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc	2340
aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc	2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt	2460
ggcctttcac tcctggctgt gcccggtggc acggtgttgc ctttactgca gcattctctgc	2520
ggctgggacg tctgggtactg tttccatctg tgctggcat ggctacctt gctgaccctg	2580

ggccggcgca gcgccaagc tctcccttat gatgccttcg tgggtgttcga taaggcgag 2640  
 agcgcggttg ctgactgggt gtataacgag ctctgagtgc ggctagagga gcggcgcggt 2700  
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgcctggcca gacactcttc 2760  
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttgtgct ggccacacg 2820  
 gacaaggta gtggcctcct gcgcaccagc ttctgctgg ctcagcagcg cctgctggag 2880  
 gaccgcaagg acgtgggtgt gttgggtgac ctgcgcctg atgcccaccg ctcccgtac 2940  
 gtgcgactgc gccagcgct ctgccgccag agtgtgtct tctggcccca tcagcccaac 3000  
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060  
 tataaccgga acttctgccg gggacctaca gcagaatag 3099

<210> 4  
 <211> 2463  
 <212> DNA  
 <213> Rattus norvegicus

<400> 4  
 atggttctct gtgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgtctg 60  
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120  
 ggctggtag actgcaactg gctcttcttg aagtctgtgc ctcaattctc tgccgcagaa 180  
 ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctgactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctcctgc cgcattacca ttgagcccaa aaccttctg 360  
 gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggg actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcaacggggc ggtgaacgtg acccgggacg ccttctctggg cttgagcaac 600  
 ctacccact tgtcccttaa gtataacaac ctacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtctataac ctcatcgta agctgggggc cgaagacctt 720  
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780  
 gccccgacc tctgtacaga atgcccgcag aagtccttg atctgcacc tcagactttc 840  
 catcacctga gccacctga aggctgggtg ctgaaggaca gttctctcca ctgctgaac 900  
 tccaagtgtt tccaggtctt ggcgaacctc tcggtgctgg acctaaagca gaactttctc 960  
 tacgagagca tcaacaaaac cagcgctttt cagaacctga cccgtctgcg caagctcgac 1020

```

ctgtccttca attactgcaa gaaggtatcg ttcgcccgcc tccacctggc aagttccttc 1080
aagagcctgg tgtcgtcgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctgggtctg cccaagctcc acacgctgca ccttcaaagt 1200
aatttcacga accagggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagac 1380
actcccgctc caaagaactt catggctcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggg gtggggccgc tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcacc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaata 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgtc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gccatttgt atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgcacc tttgtagact tactgctgga agtgcagacc 2340
aaggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460
ggc 2463

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15  
 Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30  
 Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45  
 Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60  
 Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80  
 Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110  
 Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125  
 Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140  
 Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160  
 His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175  
 Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190  
 Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205  
 Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220  
 Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705		710		715		720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu						
		725		730		735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys						
		740		745		750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr						
		755		760		765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro						
		770		775		780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile						
		785		790		795
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn						
		805		810		815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro						
		820		825		830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu						
		835		840		845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala						
		850		855		860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val						
		865		870		875
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg						
		885		890		895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro						
		900		905		910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg						
		915		920		925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu						
		930		935		940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys  
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg  
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp  
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr  
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys  
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 6  
 <211> 819  
 <212> PRT  
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110



Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe  
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu  
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys  
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr  
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro  
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile  
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn  
 805 810 815

Cys Phe Gly

<210> 7  
 <211> 3352  
 <212> DNA  
 <213> Sus scrofa

<400> 7  
 gagcacgaac atccttcact gtagctgctg cccggtctgc cagccagacc ctttgagaa 60  
 gacccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctggtgca 120  
 ggtgacagcg ctggctgcgg ctctggcca gggcaggctg cctgccttcc tgccctgtga 180  
 gctccagccc cagggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240  
 ctggcgcca gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300  
 ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360  
 gaactgcccg cgggctggcc tcagccccat gcacttcccc tgccacatga ccatcgagcc 420  
 caacaccttc ctggcctgct ccaccctgga ggagctgaac ctgagctaca acagcatcac 480  
 gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagcgcga ccaacatcct 540  
 ggtgctagac cccaccacc tcactggcct acatgccctg cgctacctgt acatggatgg 600  
 caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660  
 cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720  
 cagcctgccc cccagcctgg agaccctgct gttgtcctac aaccacattg tcacctgac 780  
 gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg 840  
 ccgctgtgac catgcccgca accctgcag ggagtgccca aaggaccacc ccaagctgca 900  
 ctctgacacc ttcagccacc tgagccgct cgaaggcctg gtgttgaaag acagtctctt 960  
 ctacaacctg gacaccaggt ggttcgagg cctggacagg ctccaagtgc tggacctgag 1020  
 tgagaacttc ctctacgact gcataccaa gaccacggcc ttccagggcc tggcccgact 1080  
 gcgcagcctc aacctgtcct tcaattacca caagaagggt tcctttgcc accctgcacct 1140  
 ggcacctcc tttgggcacc tccggtccct gaaggagctg gacatgcatg gcatcttctt 1200  
 ccgctcgctc agtgagacca cgctccaacc tctggtccaa ctgcctatgc tccagacct 1260  
 gcgcctgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg ccttccctgg 1320  
 cctgctgtac gtggacctat cggacaaccg catcagcgga gctgcaaggc cagtggccat 1380  
 tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgctccacg 1440  
 tccactggac actctccgt cagaggactt catgccaaac tgcaaggcct tcagcttcac 1500

cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc 1560  
acgcctcgag tgcctgcgcc tgagccacaa cagcatctcc caggcggtea atggctctca 1620  
gtttgtgccc ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta 1680  
tcacggggcg tcgttcacgg agctgccgag cctggaagca ctggacctca gctacaatag 1740  
ccagcccttt accatgcagg gtgtgggcca caacctcagc ttcgtggccc agctgcccgc 1800  
cctgcgctac ctacgcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg 1860  
tagcgctca ctgtgcgcc tggactttag cggcaacgat ctgagccgga tgtgggctga 1920  
gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc 1980  
ccagaaccac ctgcacaccc tcttgccagc tgccctggac aacctccca aaagcctgaa 2040  
gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgaccctcct 2100  
gcccagctg gaaaccttg acttggtgg aaaccagctg aaggccctaa gcaatggcag 2160  
cctgccatct ggcacccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt 2220  
gaacctggc tcttttgccc tggccaagca gttagaagag ctcaacctca gcgccaatgc 2280  
cctcaagaca gtggagccct cctggtttg ctcgatggtg ggcaacctga aagtcctaga 2340  
cgtgagcgcc aacctctgc actgtgcctg tggggcgacc ttcgtgggct tctgtctgga 2400  
ggtacaggct gccgtgcctg ggctgcccag ccgcgtcaag tgtggcagtc cggggcagct 2460  
ccagggccat agcatctttg cgcaagacct gcgcctctgc ctggatgaga cctctctgtg 2520  
gaactgtttt ggcatctgc tgttgcccat ggccctgggc ctggttggtc ccatgctgca 2580  
ccacctctgc ggctgggacc tctggtagct ctccacctg tgcctggcct ggctgcccc 2640  
ccgagggcag cggcggggcg cagacgcct gttctatgat gccttcgtgg tctttgacaa 2700  
agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg 2760  
ccgtggggcg cgcgcactgc gcctgtgcct ggaggagcga gactggttac ctggcaagac 2820  
gctcttcgag aacctgtgg cctcagtcta cagcagccgc aagaccctgt ttgtgctggc 2880  
ccacacggac cgtgtcagcg gcctcttgcg tgccagttc ctgctggccc agcagcgct 2940  
gctggaggac cgcaaggacg ttgtagtgt ggtgatcctg cgcgccgatg cctaccgctc 3000  
ccgtacgtg cggctgcgcc agcgctctg ccgcagagt gtccctctct ggccccacca 3060  
gccccgtgg cagggcagct tctgggcca gctgggcaca gccctgacca gggacaacca 3120  
ccacttctat aaccggaact tctgccggg cccacgaca gccgaatagc actgagtgc 3180  
agccagttg cccagcccc cctggatttg cctctctgcc tgggggtgcc caacctgctt 3240  
tgctcagcca caccactgct ctgctccctg tccccaccc cccccccag cctggcatgt 3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8  
 <211> 2457  
 <212> DNA  
 <213> Sus scrofa

<400> 8  
 atggggcccc gctgcaccct gcaccccctt tctctcctgg tgcaggtgac agcgtggct 60  
 gcggctctgg cccagggcag gctgcctgcc ttcttgccct gtgagctcca gccccacggc 120  
 ctggtgaact gcaactggct cttcctgaag tccgtgcccc acttctcggc ggcagcggcc 180  
 cgggccaacg tcaccagcct ctcttactc tccaaccgca tccaccacct gcacgactcc 240  
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaactg cccgcggct 300  
 ggctcagcc ccattgcactt cccttgccac atgaccatcg agcccaacac cttcctggcc 360  
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgaccgt gcctgcccctg 420  
 cccgactccc tcgtgtccct gtcgtgagc cgcaccaaca tcctgggtgt agaccccacc 480  
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540  
 aacccctgcc agggggcgct ggagggtgtg ccgggtgccc tcctcggcct gggcaacctc 600  
 acacatctct cactcaagta caacaatctc acggagggtgc cccgcagcct gccccccagc 660  
 ctggagaccc tgctgttgtc ctacaaccac attgtcacc tgacgcctga ggacctggcc 720  
 aatctgactg ccctgcgcgt gcttgatgtg ggggggaact gccgcgctg tgaccatgcc 780  
 cgcaaccctt gcagggagtg cccaaaggac caccccaagc tgcactctga caccttcagc 840  
 cacctgagcc gcctcgaagg cctgggtgtg aaagacagtt ctctctacaa cctggacacc 900  
 aggtggttcc gaggcctgga caggtccaa gtgctggacc tgagtgagaa cttcctctac 960  
 gactgcatca ccaagaccac ggccctccag ggccctggcc gactgcgcag cctcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttt gccacactgc acctggcacc ctcctttggg 1080  
 cacctccggt ccctgaagga gctggacatg catggcatct tcttcgctc gctcagtga 1140  
 accagctcc aacctctggt ccaactgcct atgtccaga ccctgcgcct gcagatgaac 1200  
 ttcattaacc aggccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260  
 ctatcggaca accgcatcag cggagctgca aggccagtgg ccattactag ggaggtggat 1320  
 ggtagggaga gggctctggct gccttcagga aacctcgtc cacgtccact ggacactctc 1380  
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcgg 1440  
 aacaacctgg tgacaatcca gtcggagatg tttgctcgc tctcagcct cgagtgcctg 1500

cgccctgagcc acaacagcat ctcccaggcg gtcaatggct ctcagtttgt gccgctgacc 1560  
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620  
 acggagctgc cgcgcctgga agcactggac ctcagctaca atagccagcc ctttaccatg 1680  
 cagggtgtgg gccacaacct cagcttcgtg gccagctgc ccgcccgcg ctacctcagc 1740  
 ctggcgcaaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctactgtgc 1800  
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860  
 cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920  
 accctcctgc cacgtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980  
 gacaataacc tggccttctt caactggagc agcctgacct tcctgcccac gctggaaacc 2040  
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100  
 cagctgcgga ggctggacct cagtggcaac agcatcggct ttgtgaacct tggcttcttt 2160  
 gccctggcca agcagttaga agagctcaac ctcagcgcca atgccctcaa gacagtggag 2220  
 ccctcctggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaaccct 2280  
 ctgcactgtg cctgtggggc gaccttcgtg ggcttcctgc tggaggtaca ggctgccgtg 2340  
 cctgggctgc ccagccgct caagtgtggc agtccggggc agctccaggg ccatagcatc 2400  
 tttgcgcaag acctgcgct ctgcctggat gagaccctct cgtggaactg ttttggc 2457

<210> 9

<211> 1029

<212> PRT

<213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr



305		310		315		320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg	325		330		335	
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His	340		345		350	
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu	355		360		365	
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln	370		375		380	
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn	385		390		395	400
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu	405		410		415	
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro	420		425		430	
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu	435		440		445	
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp	450		455		460	
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn	465		470		475	480
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu	485		490		495	
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly	500		505		510	
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His	515		520		525	
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln	530		535		540	

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg  
 930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala  
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
 1010 1015 1020

Gly Pro Thr Thr Ala Glu  
1025

<210> 10  
<211> 818  
<212> PRT  
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln  
 370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

gggaagtggg cgccaagcat ccttcctgc agctgcctcc caacctgccc gccagaccct 60

ctggagaagc cgcattccct gtcattggcc cctactgtgc cccgcacccc ctttctctcc 120

tgggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttctctg 180

cctgtgagct ccagcccat ggtaggtgg actgcaactg gctgttctg aagtctgtgc 240

cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc 300

gcatccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc	360
tcaagtggaa ctgcccgcg gccggcctca gcccctgca cttcccctgc cgtatgacca	420
tcgagcccaa caccttcctg gctgtgcca ccctggagga gctgaacctg agctacaacg	480
gcatcacgac cgtgcctgcc ctgcccagtt ccctcgtgtc cctgtcgtg agccacacca	540
gcatcctggg gctaggcccc acccacttca ccggcctgca cgcctgcgc tttctgtaca	600
tggacggcaa ctgctactac atgaaccctt gccgcgggc cctggagggtg gcccaggcg	660
ccctcctcgg cctgggcaac ctcacgcacc tgtcgtcaa gtacaacaac ctcacggagg	720
tgccccgcg cctgcccccc agcctggaca ccctgctgt gtcctacaac cacattgtca	780
ccctggcacc cgaggacctg gccaacctga ctgcctgcg cgtgcttgac gtgggtggga	840
actgccgcg ctgcgaccat gcccgcaacc cctgcaggga gtgcccagg aacttcccca	900
agctgcaccc tgacaccttc agtcacctga gccgcctcga aggcctgggtg ttgaaggaca	960
gttctctcta caaactagag aaagattggt tccgcggcct gggcaggctc caagtgtcgt	1020
acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga	1080
cccagctgcg cagactcaac ctgtccttca attaccaca gaagggtgtc ttcgcccacc	1140
tgcacctage gtctcctttt gggagtctgg tgtccttga gaagctggac atgcacggca	1200
tcttcttcg ctccctcacc aacatcacgc tccagtgcgt gaccggctg cccaagctcc	1260
agagtctgca tctgcagctg aacttcctca accaggccca gctcagcatc tttggggcct	1320
tcccagacct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag	1380
cggccgcctt gggggagggtg gacagcagg tggaagtctg gcgattgccc aggggcctcg	1440
ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaaagtgc aacctcaact	1500
tcaccttga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcgc	1560
tctccgcct ccagtgcctg cgcttgagcc acaacagcat ctgcaggcg gttaatggct	1620
cccagttcgt gccgtgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc	1680
tgtaccatgg gcgctcatc acggagctgc cgcagctgga ggcactggac ctgagctaca	1740
acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc	1800
cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc	1860
tcagcagcgc ctggttgcgc gccctggact tcagcggcaa ctccctgagc cagatgtggg	1920
cggagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc	1980
tgtccgagaa ccatctgcac accctcctgc ctgcctacct ggacaacctg cccaagagcc	2040



tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100  
 tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160  
 gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220  
 tcgtgatccc cggcttcttc gtccgcgcga ctccggctgat agagcttaac ctccagcgcca 2280  
 atgccctgaa gacagtggat ccctcctggg tccggttcctt agcagggacc ctgaaaatcc 2340  
 tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400  
 tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccggggc 2460  
 agctccaggg ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520  
 ccttggaactg ctttggcctc tcaactgctaa tggtagcgct gggcctggca gtgcccatgc 2580  
 tgcaccacct ctgtggctgg gacctctggg actgcttcca cctgtgtctg gcccatctgc 2640  
 cccgacggcg gcggcagcgg ggcgaggaca cctgtctcta tgatgccgtc gtgggtcttcg 2700  
 acaagggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760  
 agcgccgggg gcgcccggcg ctccgcctct gcctggagga gcgagactgg ctccctggta 2820  
 agacgtctct cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880  
 tggaccacac ggaccggggtc agcggcctcc tgcgcgccag ctctctgctg gccagcagc 2940  
 gcctgttga ggaccgcaag gacgtcgtag tgctgggtgat cctgcgcccc gccgcctatc 3000  
 ggtcccgtca cgtgcggctg cgcagcgc tctgcccga gagcgtcctc ctctggcccc 3060  
 accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120  
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180  
 tgactgccc g 3191

&lt;210&gt; 12

&lt;211&gt; 2454

&lt;212&gt; DNA

&lt;213&gt; Bos taurus

&lt;400&gt; 12

atgggccctt actgtgcccc gcacccctt tctctcctgg tgcaggcggc ggcaactggca 60  
 gcggccctgg ccgagggcac cctgcctgcc ttcttgccct gtgagctcca gccccatggt 120  
 cagggtggact gcaactggct gttcctgaag tctgtgccgc acttttcggc tggagcccc 180  
 cgggccaatg tcaccagcct ctcttaatc tccaaccgca tcaccactt gcatgactct 240  
 gacttcgtcc acctgtccaa cctgcgggct ctcaacctca agtggaactg cccgccggcc 300  
 ggcctcagcc ccatgcactt cccctgccgt atgaccatcg agcccaacac ctctcctggct 360

gtgcccaccc	tggaggagct	gaacctgagc	tacaacggca	tcacgaccgt	gcctgccctg	420
cccagttccc	tcgtgtccct	gtcgctgagc	cacaccagca	tcctggtgct	aggccccacc	480
cacttcaccg	gcctgcacgc	cctgcgcttt	ctgtacatgg	acggcaactg	ctactacatg	540
aacctctgcc	cgcgggccct	ggaggtggcc	ccaggcgccc	tcctcggcct	gggcaacctc	600
acgcacctgt	cgctcaagta	caacaacctc	acggaggtgc	cccgcgcct	gccccccagc	660
ctggacaccc	tgctgtgtgc	ctacaaccac	attgtcacc	tggcacccga	ggacctggcc	720
aacctgactg	ccctgcgcgt	gcttgacgtg	ggtgggaact	gccgcgcgtg	cgaccatgcc	780
cgcaaccct	gcagggagtg	cccaaagaac	ttccccaagc	tgcaccctga	caccttcagt	840
cacctgagcc	gcctcgaagg	cctggtgttg	aaggacagtt	ctctctacaa	actagagaaa	900
gattggttcc	gcggcctggg	caggctccaa	gtgctcgacc	tgagtgagaa	cttcctctat	960
gactacatca	ccaagaccac	catcttcaac	gacctgaccc	agctgcgcag	actcaacctg	1020
tccttcaatt	accacaagaa	ggtgtccttc	gccacctgc	acctagcgtc	ctcctttggg	1080
agtctggtgt	ccctggagaa	gctggacatg	cacggcatct	tcttcgcctc	cctcaccaac	1140
atcacgctcc	agtcgctgac	ccggctgccc	aagctccaga	gtctgcatct	gcagctgaac	1200
ttcatcaacc	aggcccagct	cagcatcttt	ggggccttcc	cgagcctgct	cttcgtggac	1260
ctgtcggaca	accgcatcag	cggagccgcg	acgccagcgg	ccgccctggg	ggaggtggac	1320
agcaggggtg	aagtctggcg	attgcccagg	ggcctcgctc	caggcccgct	ggacgcgcgc	1380
agctcaaagg	acttcatgcc	aagctgcaac	ctcaacttca	ccttggaacct	gtcacggaac	1440
aacctggtga	caatccagca	agagatgttt	accgcctct	cccgcctcca	gtgcctgcgc	1500
ctgagccaca	acagcatctc	gcaggcggtt	aatggctccc	agttcgtgcc	gctgaccagc	1560
ctgcgagtgc	tcgacctgtc	ccacaacaag	ctggacctgt	accatgggcg	ctcattcacg	1620
gagctgccgc	agctggaggc	actggacctc	agctacaaca	gccagccctt	cagcatgcag	1680
ggcgtggggc	acaacctcag	cttcgtggcc	cagctgccct	ccctgcgcta	cctcagcctt	1740
gcgcacaatg	gcatccacag	ccgcgtgtca	cagaagctca	gcagcgctc	gttgcgcgcc	1800
ctggacttca	gcggcaactc	cctgagccag	atgtgggccc	aggagacct	ctatctctgc	1860
tttttcaaag	gcttgaggaa	cctggtccag	ctggacctgt	ccgagaacca	tctgcacacc	1920
ctcctgcctc	gtcacctgga	caacctgccc	aagagcctgc	ggcagctgcg	tctccgggac	1980
aataacctgg	ccttcttcaa	ctggagcagc	ctgaccgtcc	tgccccggct	ggaagccctg	2040
gatctggcag	gaaaccagct	gaaggccctg	agcaacggca	gcctgccgcc	tggcatccgg	2100
ctccagaagc	tggacgtgag	cagcaacagc	atcggcttcg	tgatccccgg	cttcttcgtc	2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220  
 tcctggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caaccgctc 2280  
 cactgcgect gcggggcggc ctttgtggac ttctgtctgg agagacagga ggccgtgccc 2340  
 gggctgtcca ggcgcgtcac atgtggcagt ccgggccagc tccagggccg cagcatcttc 2400  
 acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13  
 <211> 1031  
 <212> PRT  
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro  
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe  
 260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415  
 Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430  
 Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445  
 Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460  
 Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480  
 Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495  
 Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510  
 Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525  
 Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540  
 Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560  
 Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575  
 Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590  
 Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605  
 Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620  
 Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met  
 820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
 835 840 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp  
 850 855 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865                                      870                                      875                                      880  
 Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
    885                                      890                                      895  
 Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
    900                                      905                                      910  
 Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
    915                                      920                                      925  
 Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu  
    930                                      935                                      940  
 Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
    945                                      950                                      955                                      960  
 Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser  
    965                                      970                                      975  
 Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe  
    980                                      985                                      990  
 Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
    995                                      1000                                      1005  
 Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe  
    1010                                      1015                                      1020  
 Cys Arg Gly Pro Thr Met Ala Glu  
    1025                                      1030  
  
 <210> 14  
 <211> 820  
 <212> PRT  
 <213> Equus caballus  
  
 <400> 14  
  
 Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1                                      5                                      10                                      15  
  
 Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
    20                                      25                                      30  
  
 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35	40	45
Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn		
50	55	60
Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp		
65	70	75
Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp		
85	90	95
Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met		
100	105	110
Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu		
115	120	125
Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser		
130	135	140
Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro		
145	150	155
Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly		
165	170	175
Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro		
180	185	190
Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr		
195	200	205
Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr		
210	215	220
Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu		
225	230	235
Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg		
245	250	255
Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe		
260	265	270



Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly  
 820

<210> 15  
 <211> 3391  
 <212> DNA  
 <213> Equus caballus

<400> 15  
 ctctgttctc tgagctgttg ccgctgaag ggactgcgag cacaagcat cctcctctgc 60  
 agctgctgcc cagtgtgcca gctggaccct ctggatcatc tcccactccc tgatcatgggc 120  
 ccttgccatg gtgccttgca gccctgtct ctctgggtgc aggcggccat gctggccgtg 180  
 gctctggccc aaggcaccct gcctcccttc ctgcccgtg agctccagcc ccacggcctg 240  
 gtgaactgca actggctggt cctgaagtcc gtgcccact tctcagcagc agcaccctgg 300  
 gacaatgtca ccagcctttc cttgctctcc aaccgcatcc accacctcca cgactccgac 360  
 tttgccaac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc 420  
 ctacgcccga tgcacttccc ctgccatag accatcgagc ccaacacttt cctggctgta 480  
 cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540  
 agctccctcg tgtccctgat cctgagccgc accaacatcc tgcagctaga cccaccagc 600  
 ctacggggcc tgcatgccct gcgcttccca tacatggatg gcaactgcta ctacaagaac 660  
 ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc 720  
 cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc cctagcctg 780  
 gagtacctgc tgttgtccta caaccacatt gtcaccctgg cacctgagga cctggccaat 840  
 ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900  
 aaccctgcg tggagtgcgc acataaatcc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga	1020
tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac	1080
tgcatcacca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgtcc	1140
ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc	1200
ctgctctccc tgcaggaact ggacatgcat ggcattctct tccgctcact cagccagaag	1260
acgtccagc cactggcccgc cctgcccattg ctccagcgtc tgtatctgca gatgaacttc	1320
atcaaccagg cccagctcgg catcttcaag gacttccttg gtctgcgcta catagacctg	1380
tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt	1440
gggaagaagg tctggctgac atccagggac ctactccag gccactgga cccccccagc	1500
tctgaggact tcatgccaaag ctgcaagaac ctacagcttca ccttggaact gtcacggaac	1560
aacctggtaa cagtccagcc agagatgttt gccagctct cgcgcctcca gtgcctgcgc	1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc	1680
ctgcagggtgc tggacctgtc ccataacaaa ctggacctgt accatgggag ctcgtttacg	1740
gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg	1800
ggtgtggggc acaacctcag ctttgtggcc cagctgccca ccctgcgcta cctcagcctg	1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtggggc	1920
ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc	1980
ttcttccaag gcctgagaag cctaattccg ctagacctgt cccagaatcg tctgcatacc	2040
ctcctgccat gcacctggg caacctcccc aagagcttgc agctgctgcg tctccgtaac	2100
aattacctgg ccttcttcaa ttggagcagc ctgacctcc tgcccaacct ggaaacctg	2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag	2220
ctccagaggc tggacgtcag caggaacagc atcatcttcg tggtccttg cttctttgct	2280
ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc	2340
tcctggtttg gtttcctagc aggtccctt gaagtcctag atgtgagcgc caacctctg	2400
cactgcgcct gtggggcagc ctttgtggac ttctgctgc aggttcaggc tgccgtgcct	2460
ggtctgcca gccgcgtcaa gtgtggcagt ccgggcccag tccagggccg cagcatcttc	2520
gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctctctca	2580
ttgtggttg tggccctggg cctggccattg cctatgttgc accacctctg cggtgggagc	2640
ctctggtact gcttcacct gggcctggcc tggctgcccc ggcgggggtg gcagcggggc	2700

gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760  
 gactgggtgt acaatgaact gcgggtgcgg ctagaggagc gccgtgggcg ccgggcgctc 2820  
 cgctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880  
 gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940  
 ggcctcttgc gtgccagctt cctgctggcc cagcagcgctc tgctggagga ccgcaaggac 3000  
 gttgtggtgc tggtaatcct gagccctgac gcccgccggtt cccgttacgt gcggctgcgc 3060  
 cagcgcctct gccgccagag tgtcctcttc tggccccacc agcctagtgg ccagcgcagc 3120  
 ttctgggccc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180  
 ttctgccggg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaaccc 3240  
 ccagccctga ccttgccctct ctgcctatga tgcccagtct gcctcactct gtgacgcccc 3300  
 tgctctgcct ccgccaccct caccctggc atacagcagg cactcaataa atgccactgg 3360  
 caggccaaac agccaaaaa aaaaaaaaaa a 3391

<210> 16

<211> 2460

<212> DNA

<213> Equus caballus

<400> 16

atgggccctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60  
 gccgtggctc tggcccaagg caccctgcct ccttctctgc cctgtgagct ccagccccac 120  
 ggctgtgtga actgcaactg gctgttctctg aagtccgtgc cccacttctc agcagcagca 180  
 ccccgggaca atgtcaccag ccttctcttg ctctccaacc gcattccacca cctccacgac 240  
 tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaatggaa ctgcccgcca 300  
 gccggcctca gcccctatgca cttcccctgc cacatgacca tcgagcccaa cactttctctg 360  
 gctgtacca ccctggagga gctgaacctg agctacaacg gcattcacgac tgtgcctgcc 420  
 ctgcccagct ccctcggtgc cctgatctctg agccgcacca acatcctgca gctagacccc 480  
 accagcctca cgggcctgca tgccctgcgc ttctataca tggatggcaa ctgctactac 540  
 aagaaccctt gcggggcggc cctggagggtg gcccagggcg cctccttgg cctgggcaac 600  
 ctccccacc tgtcactcaa gtacaacaac ctcaaacgg tgccccgcag cctgccccct 660  
 agcctggagt acctgctgtt gtcctacaac cacattgtca ccctggcacc tgaggacctg 720  
 gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgccg ctgtgaccat 780  
 gcacgcaacc cctgcgtgga gtgcccacat aaattcccc agctgcactc cgacaccttc 840

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac 900  
 cccagatggg tccgtggcct gggcaacctc acagtgtctg acctgagtga gaacttcctc 960  
 tacgactgca tcaccaaaac caaggcattc cagggcctgg cccagctgcg aagactcaac 1020  
 ttgtccttca attaccataa gaagggtgtcc ttgcgccacc tgacgtggc accctccttc 1080  
 gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttccg ctactcagc 1140  
 cagaagacgc tccagccact ggcccgctg cccatgtctc agcgtctgta tctgcagatg 1200  
 aacttcatca accaggccca gctcggcatc ttcaaggact tccctgggtc gcgtacata 1260  
 gacctgtcag acaaccgat cagtggagct gtggagccgg tggccaccac aggggaggtg 1320  
 gatggtggga agaaggtctg gctgacatcc agggacctca ctccaggccc actggacacc 1380  
 cccagctctg aggacttcat gccaaagtgc aagaacctca gcttcacctt ggacctgtca 1440  
 cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc 1500  
 ctgcgcctga gccacaacag catctcgcag gcggtcaatg gctcacagtt cgtgccactg 1560  
 accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg 1620  
 ttacggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc 1680  
 atgcggggtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgtacctc 1740  
 agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctgcag cacctcgtg 1800  
 tgggcctgg acttcagcgg caattccctg agccagatgt gggctgaggg agaccttat 1860  
 ctccgttct tccaaggcct gagaagccta atccggctag acctgtacca gaatcgtctg 1920  
 cataccctcc tgccatgcac cctgggcaac ctccccaaga gcttgcagct gctgcgtctc 1980  
 cgtaacaatt acctggcctt cttcaattgg agcagcctga cctcctgcc caacctggaa 2040  
 acctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc 2100  
 acccagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggg ccttggttc 2160  
 tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgcct caggacagag 2220  
 gagccctcct ggtttggttt cctagcaggc tcccttgaag tcctagatgt gagcgccaac 2280  
 cctctgcact gcgcctgtgg ggcagcctt gtggacttcc tgctgcaggt tcaggctgcc 2340  
 gtgcctggtc tgcccagccg cgtcaagtgt ggcagtccg gccagctcca gggccgcagc 2400  
 atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttgg 2460

&lt;210&gt; 17

&lt;211&gt; 1029

&lt;212&gt; PRT

&lt;213&gt; Ovis aries

&lt;400&gt; 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460



Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930                      935                      940  
 Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945                      950                      955                      960  
 Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
                     965                      970                      975  
 Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
                     980                      985                      990  
 His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala  
                     995                      1000                      1005  
 Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
                     1010                      1015                      1020  
 Gly Pro Thr Thr Ala Glu  
                     1025  
 <210> 18  
 <211> 818  
 <212> PRT  
 <213> Ovis aries  
 <400> 18  
 Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1                      5                      10                      15  
 Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
                     20                      25                      30  
 Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
                     35                      40                      45  
 Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
                     50                      55                      60  
 Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65                      70                      75                      80  
 Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
                     85                      90                      95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn		
115	120	125
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu		
130	135	140
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr		
145	150	155
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn		
165	170	175
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly		
180	185	190
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn		
195	200	205
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu		
210	215	220
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala		
225	230	235
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg		
245	250	255
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro		
260	265	270
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu		
275	280	285
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg		
290	295	300
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr		
305	310	315
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg		
325	330	335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

&lt;210&gt; 19

&lt;211&gt; 3199

&lt;212&gt; DNA

&lt;213&gt; Ovis aries

&lt;400&gt; 19

```

gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc      60
cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgccc cgcaccccct      120
ttctctcctg gtgcaggcgg cggcgtctggc agcagccctg gcccagggca ccctgcctgc      180
cttcctgccc tgtgagctcc agccccgggg taaggatgaac tgcaactggc tgttcctgaa      240
gtctgtgccc cgtttttcgg ccggagcccc ccgggccaat gtcaccagcc tctccttaat      300
ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcgggt      360
cctcaacctc aagtggaact gcccgccggc cggcctcagc cccatgcact tcccctgccg      420
catgaccatc gagcccaaca ccttcctggc tgtgcccacc ctggaggagc tgaacctgag      480
ctacaatggc atcacgaccg tgcttgccct gcccagttct ctcgatatccc tgtcgctgag      540
ccgcaccagc atcctggtgc taggccccac ccacttcacc ggcctgcacg ccctgcgctt      600
tctgtacatg gacggcaact gctactataa gaaccctgc cagcaggccg tggagggtggc      660
cccaggcgcc ctcttgggc tgggcaacct cagcacctg tcgctcaagt acaacaacct      720
cacggagggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca      780
catcatcacc ctggcaccgg aggacctggc caatctgact gccctgcgtg tgcttgatgt      840
gggcggggaac tgccgcccgt gcgaccacgc ccgcaacccc tgcagggagt gcccaaagaa      900
cttccccaag ctgcacctg acaccttcag ccacctgagc cgcctcgaag gcctgggtgtt      960
gaaggacagt tctctctaca aactagagaa agactggttc cgcggcctgg gcaggctcca     1020
agtgtctgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag     1080
gaacctgacc cagctgcgca gactcaacct gtccttcaat taccacaaga aggtgtcctt     1140
cgccacctg caactggcac cctcctttgg gggcctggtg tccctggaga agctggacat     1200
gcacggcatc ttcttcgct ccctcaccaa caccacgctc cggccgctga ccagctgcc     1260
caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt     1320
tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc     1380
gaggccggtg gccgccctcg gggagggtgga cagcggggtg gaagtctggc ggtggcccag     1440

```

```

gggcctcgct ccaggcccg tggccgccgt cagcgcaaag gacttcatgc caagctgcaa 1500
cctcaacttc accttgacc tgtcacggaa caacctggtg acgatccagc aggagatggt 1560
taccgccttc tccgcctcc agtgccctgc cctgagccac aacagcatct cgcaggcggt 1620
taatggctcg cagttcgtgc cgctgacctg cctgcgagtg ctgcacctgt cctacaacaa 1680
gctggacctg taccatgggc gctcgttcac ggagctgccg cagctggagg cactggacct 1740
cagctacaac agccagccct tcagcatgca gggcgtaggc cacaacctca gcttcgtggc 1800
ccagctgccg tccctgcgt acctcagcct tgcgcacaac ggcatccaca gccgcgtgtc 1860
acagaagctc agcagcgct cgctgcgcgc cctggacttc agcggcaact ccctgagcca 1920
gatgtgggcc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctgggtcca 1980
gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc 2040
caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag 2100
cctgactgtt ctgcccagc tggaagccct ggatctggcg ggaaccagc tgaaggccct 2160
gagcaacggc agcctgccac ctggcacccg gctccagaag ctggacgtga gcagcaacag 2220
catcggttt gtgacctctg gcttctttgt ccttgccaac cggctgaaag agcttaacct 2280
cagcgccaac gccctgaaga cagtggatcc cttctggttc ggtcgcttaa cagagacct 2340
gaatatacta gacgtgagcg ccaaccgct cactgtgcc tgcggggcg cctttgtgga 2400
cttctgtctg gagatgcagg cggccgtgcc tgggctgtcc aggcgcgtca cgtgtggcag 2460
tccgggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga 2520
gacctctctc ttggactgt ttggcttctc gctgctaatg gtggcgctgg gcctggcggt 2580
gcccattgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc 2640
ccatttgccc cgacggcggc ggcagcgggg cgaggacacc ctgctctacg atgcctctgt 2700
ggctctcgac aaggcgaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca 2760
gctggaggag cgcgcgggc gccgggcgt ccgcctctgc ctggaggagc gagactggct 2820
ccctggcaag acgctcttcg agaacctgtg ggccctcggtc tacagcagcc gtaagaccat 2880
gttcgtgtg gaccacacgg accgggtcag tggcctcctg cgcgccagct tcctgtggc 2940
ccagcagcgc ctgttgagg accgcaagga tgcgtggtg ctggtgatcc tgcgccccgc 3000
cgcctaccgg tccgctacg tgcggctgc ccagcgctc tgcgccaga gcgtcctct 3060
ctggccccac cagccagtg gccaggtag cttctgggccc aacctgggca tggccctgac 3120
cagggacaac cgccacttct ataaccggaa cttctgccgg ggccccacga cagccgaata 3180

```



gcacagagtg actgcccag

3199

&lt;210&gt; 20

&lt;211&gt; 2454

&lt;212&gt; DNA

<213> *Ovis aries*

&lt;400&gt; 20

atggggccct actgtgcccc gcacccctt tctctcctgg tgcaggcggc ggcgctggca 60  
 gcagccctgg cccagggcac cctgcctgcc ttctgcccct gtgagctcca gcccgggggt 120  
 aaggtgaact gcaactggct gttcctgaag tctgtgcccgc gcttttcggc cggagccccc 180  
 cggggccaatg tcaccagcct ctcttaatac tccaaccgca tccaccactt gcacgactct 240  
 gacttogtcc acctgtocaa cctgcgggtc ctcaacctca agtggaactg cccgccggcc 300  
 ggctcagcc ccatgcactt cccctgcccgc atgaccatcg agcccaacac ctctctggct 360  
 gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgccctg 420  
 cccagttctc tcgtatccct gtgcctgagc cgcaccagca tcctgggtgct agggcccacc 480  
 cacttcaccg gcctgcaagc cctgcgcttt ctgtacatgg acggcaactg ctactataag 540  
 aacccttgcc agcaggccgt ggaggtggcc ccaggcgccc tccttggcct gggcaacctc 600  
 acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgccgcct gccccccagc 660  
 ctggacaccc tgctgctgtc ctacaaccac atcatcacc tggcaccoga ggacctggcc 720  
 aatctgactg ccctgcgtgt gcttgatgtg ggcgggaact gccgccgctg cgaccacgcc 780  
 cgcaaccctc gcagggagtg cccaaagaac ttccccaagc tgcaccctga caccttcagc 840  
 cacctgagcc gcctcgaagg cctgggtgtg aaggacagtt ctctctacaa actagagaaa 900  
 gactggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa ctctctctat 960  
 gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctcttttggg 1080  
 ggctgggtgt ccctggagaa gctggacatg cacggcatct tcttccgctc cctcaccaac 1140  
 accacgctcc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac 1200  
 ttcatcaacc aggcagagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac 1260  
 ctgtcggaca accgcatcag cggagctgcg aggcgggtgg ccgccctcgg ggaggtggac 1320  
 agcgggggtg aagtctggcg gtggcccagg ggcctcgctc caggcccgtc ggccgccgtc 1380  
 agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac 1440  
 aacctgggtg cgatccagca ggagatgttt accgcctct cccgcctcca gtgcctgcgc 1500

ctgagccaca acagcatctc gcaggcgggtt aatggctcgc agttcgtgcc gctgacccgc 1560  
 ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtggggc acaacctcag cttcgtggcc cagctgccgt ccctgcgcta cctcagccctt 1740  
 gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgctc gctgcgcgcc 1800  
 ctggacttca gcggcaactc cctgagccag atgtggggcg agggagacct ctatctctgc 1860  
 ttcttcaaag gcttgaggaa cctggtccag ctggacctgt ccaagaacca cctgcacacc 1920  
 ctctgcctc gtcacctgga taacctgccc aagagcctgc ggcagctgcg tctccgggac 1980  
 aataacctgg ccttcttcaa ctggagcagc ctgactgttc tgcccagct ggaagccctg 2040  
 gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccgcg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggtcttg tgaccctgg cttctttgtc 2160  
 cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220  
 ttctggttcg gtcgcttaac agagaccctg aatatcctag acgtgagcgc caaccgcctc 2280  
 cactgtgcct gcggggcggc ctttgtggac ttctgtctgg agatgcaggc ggccgtgcct 2340  
 gggctgtcca ggcggtcac gtgtggcagt ccggggccagc tccagggccg cagcatcttc 2400  
 gcacaggacc tgccctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21  
 <211> 1032  
 <212> PRT  
 <213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

- 60 -

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545		550		555		560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu						
	565			570		575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg						
	580			585		590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser						
	595			600		605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg						
	610			615		620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn						
	625			630		635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser						
	645			650		655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp						
	660			665		670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly						
	675			680		685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln						
	690			695		700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro						
	705			710		715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala						
	725			730		735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly						
	740			745		750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys						
	755			760		765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro						
	770			775		780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
 805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu  
 820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys  
 835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly  
 850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
 900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
 915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser  
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala  
1025 1030

<210> 22  
<211> 822  
<212> PRT  
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430



Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro  
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu  
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg  
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser  
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg  
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn  
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser  
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660                                      665                                      670  
 Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly  
           675                                      680                                      685  
 Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln  
           690                                      695                                      700  
 Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro  
 705                                      710                                      715                                      720  
 Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala  
                                     725                                      730                                      735  
 Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly  
                                     740                                      745                                      750  
 Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys  
           755                                      760                                      765  
 Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro  
           770                                      775                                      780  
 Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785                                      790                                      795                                      800  
 Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
                                     805                                      810                                      815  
 Ser Trp Val Cys Phe Ser  
                                     820

&lt;210&gt; 23

&lt;211&gt; 3334

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 23

```

aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca      60
gaccctctgg agaagcccc gtcacctgtc atgggcccct gccgtggcgc cctgcacccc      120
ctgtctctcc tgggtcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct      180
gccttcctgc cctgtgagct ccagcccat ggctgggtga actgcaactg gctgttcctc      240
aagtccgtgc cccgcttctc ggcagctgca cccgcggta acgtcaccag cctttccttg      300

```

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtctcaatc tcaagtggaa ctgcccgccc gccagcctca gcccacatgca ctttcctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcca ccctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccggc ctgcccagtt cgcttgtgtc cctgtccctg	540
agccgcacca acatcctggg gctggaccct gccaccctgg caggccttta tgccctgcgc	600
ttcctgttcc tggatggcaa ctgctactac aagaaccctt gccagcagga cctgcaggtg	660
gcccaggtg ccctcctggg cctgggcaac ctcacacacc tgtcactcaa gtacaacaac	720
ctcacctgtg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtcctacaac	780
cacatcatca ccctggcacc tgaggacctg gccaatotga ctgccctgcg tgctcctgat	840
gtgggtggga actgtcgccg ctgtgaccat gcccgtaacc cctgcaggga gtgccccaa	900
ggcttcccc agctgcaccc caacaccttc ggccacctga gccacctga aggcctgggtg	960
ttgagggaca gctctctcta cagcctggac ccaggtgggt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttctg tatgactgca tcacaaaaac caaagccttc	1080
tacggcctgg cccggctgcg cagactcaac ctgtccttca attatcataa gaagggtgcc	1140
tttgcccacc tgcatctggc atcctccttc gggagcctac tgtccctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccacgc tccagtcgct ggcccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggcca gctcagcatc	1320
ttcggcgcct tccctggact gcggtacgtg gacttgtcag acaaccgcat cagtggagct	1380
gcagagcccg cggctgccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtcccggt accttgctct gggcccaactg ggcaaccccg gctcagaggc cttcatgccg	1500
agctgcagga ccctcaactt caccttgga cgtgtctcga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggct ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcgttca cggagctgcc gcggctggag	1740
gccttggaac tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agccctgcgc tacctcagcc tggcgcacaa tggcatccac	1860
agccgcgtgt cccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
acctgagcc agatgtgggc cgagggagac ctctatctcc gcttcttcca aggcctgaga	1980
agcctgggtc agctggacct gtcccagaat cgctgcata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct gcggctcctg cggtccgtg acaattacct ggctttcttc	2100

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160  
ctgaaggccc tgagcaatgg cagcttgccc aacggcaccc agctccagag gctggacctc 2220  
agcggcaaca gcatcggtt cgtggtcccc agcttttttg ccctggccgt gaggcttcga 2280  
gagctcaacc tcagcgcaa cgccctcaag acggtggagc cctcctgggt tggttccctg 2340  
gcgggtgccc tgaaagtcct agacgtgacc gccaacccct tgcattgcgc ttgcggcgca 2400  
accttcgtgg acttcttgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc 2460  
aagtgcggca gcccggtcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520  
tgcctggacg aagcgtcttc ctgggtctgt ttcagcctct cgtgctggc tgtggccctg 2580  
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttcac 2640  
ctgtgcctgg cctggctgcc ccggcggggg cggcggcggg gtgtggatgc cctggcctat 2700  
gacgccttcg tggctctcga caaggcgag agctcggtgg cggactgggt gtacaatgag 2760  
ctgcgggtac agctagagga gcgcgtggg cgccggcggc tacgcctgtg tctggaggaa 2820  
cgtgactggg taccggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880  
cgcaagacgc tgtttgtgct ggcccgacg gacagagtca gcggcctcct gcgtgccagc 2940  
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggg gctggtgatc 3000  
ctgtgccccg acgcccaccg ctcccgtat gtgcggctgc gccagcgct ctgccgccag 3060  
agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc 3120  
acggccctga ccagggacaa ccggcacttc tacaaccaga acttctgccg gggccccacg 3180  
acagcctgat aggcagacag ccagcacct tcgcgcccct acaccctgcc tgtctgtctg 3240  
ggatgcccga cctgctggct ctacaccgcc gctctgtctc ccctacacc agccctggca 3300  
taaagcgacc gctcaataaa tgctgctggg agac 3334

&lt;210&gt; 24

&lt;211&gt; 2466

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 24

atggggccct gccgtggcg cctgcacccc ctgtctctcc tggtcaggg tgccgcgcta 60  
gccctggccc tggcccaggg caccctgcct gccttctgc cctgtgagct ccagcccat 120  
ggcctgggtga actgcaactg gctgttcctc aagtccgtgc ccgcttctc ggcagctgca 180  
ccccgcggtg acgtcaccag cctttccttg tactccaacc gcatccacca cctccatgac 240  
tatgactttg tccacttcgt ccacctgcgg cgtctcaatc tcaagtggaa ctgcccggcc 300

gccagcctca gcccacatgca ctttccctgt cacatgacca ttgagcccaa caccttcctg 360  
 getgtgccc cccatagagga cctgaatctg agctataaca gcatcaogac tgtgcccgcc 420  
 ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggt gctggaccct 480  
 gccaccctgg caggccttta tgccctgcgc ttctgttcc tggatggcaa ctgctactac 540  
 aagaaccctt gccagcaggc cctgcagggt gccccagggt ccctcctggg cctgggcaac 600  
 ctcacacacc tgtcactcaa gtacaacaac ctcaccgtgg tgccgcgggg cctgcccccc 660  
 agcctggagt acctgctctt gtccataaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaatctga ctgccctgcg tgtcctcgat gtgggtggga actgtcgccg ctgtgaccat 780  
 gcccgtaacc cctgcaggga gtgccccaa ggttcccc agctgcaccc caacaccttc 840  
 ggccacctga gccacctga aggcctgggt ttgagggaca gctctctcta cagcctggac 900  
 ccaggtggt tccatggcct gggcaacctc atgggtgctg acctgagtga gaacttcctg 960  
 tatgactgca tcacaaaaac caaagccttc tacggcctgg ccggtctgcg cagactcaac 1020  
 ctgtccttca attatcataa gaaggtgtcc ttgcccacc tgcactggc atcctccttc 1080  
 gggagcctac tgtccctgca ggagctggac atacatggca tcttcttcg ctgcctcagc 1140  
 aagaccacgc tccagtcgct ggccacctg cccatgctcc agcgtctgca tctgcagttg 1200  
 aactttatca gccaggccca gctcagcatc ttgggcgcct tccctggact gcggtacgtg 1260  
 gacttgtcag acaaccgcat cagtggagct gcagagcccg cggctgccac aggggaggtg 1320  
 gaggcagact gtggggagag agtctggcca cagtcccggt accttgctct gggcccaactg 1380  
 ggcacccccg gctcagaggc cttcatgccg agctgcagga ccctcaactt caccttggac 1440  
 ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcgcgcctc 1500  
 cagtgcctgg gcctgagcca caacagcatc tcgcaggcgg tcaatggctc gcagttcgtg 1560  
 cctctgagca acctgcgggt gctggacctg tccataaca agctggacct gtaccacggg 1620  
 cgctcgttca cggagctgcc gcggctggag gccttggacc tcagctaaa cagccagccc 1680  
 ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740  
 tacctcagcc tggcgacaaa tggcatccac agccgcgtgt ccagcagct ccgcagcgc 1800  
 tcgtccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgaggagac 1860  
 ctctatctcc gcttcttcca aggcctgaga agcctggttc agctggacct gtcccagaat 1920  
 cgctgcata ccctcctgcc acgcaacctg gacaacctc ccaagagcct gcggctcctg 1980  
 cggctccgtg acaattacct ggctttcttc aactggagca gcctggccct cctaccaag 2040

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100  
 aacggcacccc agctccagag gctggacctc agcggcaaca gcatcggtt cgtgggtcccc 2160  
 agcttttttg ccttgccgt gaggttcga gagctcaacc tcagcgccaa cgcctcaag 2220  
 acggtggagc cctcctggtt tggttccctg gcgggtgccc tgaaagtcct agacgtgacc 2280  
 gccaacccct tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340  
 gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400  
 cgcagcatct tcgcacagga cctgcgcctc tgctggacg aagcgctctc ctgggtctgt 2460  
 ttcagc 2466

<210> 25  
 <211> 1031  
 <212> PRT  
 <213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe



610                                      615                                      620  
 Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625                                      630                                      635                                      640  
 His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg  
 645                                      650                                      655  
 Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660                                      665                                      670  
 Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln  
 675                                      680                                      685  
 Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln  
 690                                      695                                      700  
 Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe  
 705                                      710                                      715                                      720  
 Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725                                      730                                      735  
 Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu  
 740                                      745                                      750  
 Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala  
 755                                      760                                      765  
 Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
 770                                      775                                      780  
 Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785                                      790                                      795                                      800  
 Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
 805                                      810                                      815  
 Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val  
 820                                      825                                      830  
 Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
 835                                      840                                      845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly Ala Asp  
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala  
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu  
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser  
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu  
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe  
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 26  
 <211> 820  
 <212> PRT  
 <213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
                   20                                  25                                  30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
           35                                  40                                  45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
       50                                  55                                  60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65                                  70                                  75                                  80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
                   85                                  90                                  95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
                   100                                  105                                  110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
           115                                  120                                  125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
       130                                  135                                  140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145                                  150                                  155                                  160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
                   165                                  170                                  175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
           180                                  185                                  190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
       195                                  200                                  205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
       210                                  215                                  220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225                                  230                                  235                                  240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
           245                                  250                                  255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
 610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg  
 645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725

730

735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu  
 740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly  
 820

<210> 27  
 <211> 3235  
 <212> DNA  
 <213> Felis catus

<400> 27  
 aggggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60  
 ctctggagaa gccccactc cctgtcatgg gccctgcc tggcgccctg caccctgt 120  
 ctctcctggt gcaggctgcc gcgctggccg tggccctggc ccagggcacc ctgcctgcct 180  
 ttctgccctg tgagctccag cgccacggcc tggatgaattg cgactggctg ttctcaagt 240  
 ccgtgcccc a t t t c t c g g c g g c a g c g c c c g t g g t a a c g t c a c c a g c c t t t c c c t g t a c t 300  
 ccaaccgcat ccaccactc cagcactccg actttgtcca cctgtccagc ctgcggcgctc 360  
 tcaacctcaa atggaactgc ccaccgcc gccctagccc catgcacttc ccctgtcaca 420  
 tgaccattga gccccacacc ttctggccg tgcccaccct ggaggagctg aacctgagct 480  
 acaacagcat cagcacagta ccgcccctgc ccagttccct cgtgtccctg tccttgagcc 540  
 gtaccaacat cctggtgctg gaccctgcc accctgcagg gctgcactcc ctgcgctttc 600  
 tgttcctgga tggcaactgc tactacaaga accctgccc gcaggccctg cagggtggccc 660  
 cggcgccct ccttggcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca 720  
 ctgcggtgcc ccgcggcctg cccccagcc tggagtacct gctattgtcc tacaaccaca 780

tcatacacctt ggcacctgag gacctggcca acctgaccgc cctgcgtgtg ctcgatgtgg	840
gtgggaactg ccgtcgtgtg gaccacgccc gcaaccctg tatggagtgc cccaagggtc	900
tcccgacact gcacctgac accttcagcc acctgaacca cctcgaaggc ctggtgttga	960
aggacagctc tctctacaac ctgaacccca gatgggttcca tgccctgggc aacctcatgg	1020
tgctggacct gagtgagaac ttcctatatg actgcatcac caaaaccaca gccttccagg	1080
gcctggccca gctgcgcaga ctcaacttgt ctttcaatta ccacaagaag gtgtcctttg	1140
cccacctgca tctggcgccc tccttcggga gcctgctctc cctgcagcag ctggacatgc	1200
atggcatctt cttccgctcg ctacgcgaga ccacgctccg gtcgctggtc cacctgccc	1260
tgctccagag tctgcacctg cagatgaact tcataatca ggcccagctc agcatcttcg	1320
gggccttccc tggcctgcga tacgtggacc tgtcagaaa ccgcataagt ggagccatgg	1380
agctggcggc tgccacgggg gaggtggatg gtggggagag agtcgggctg ccatctgggg	1440
acctagctct gggcccaccg ggcacccta gctccgaggg ctcatgcca ggctgcaaga	1500
ccctcaactt caccttgga cgtgcacgga acaacctagt gacaatccag ccagagatgt	1560
ttgcccggt ctcgcgcctc cagtgcctgc tcctgagccg caacagcatc tcgcaggcag	1620
tcaacggctc acaatttatg ccgctgacca gcctgcaggt gctggacctg tcccataaca	1680
agctggacct gtacctggg cgctctttca cggagctgcc gcggtggag gccctggacc	1740
tcagctacaa cagccagccc ttcagcatgc agggcgtggg tcacaacctc agctttgtgg	1800
cacagctgcc ggccctgcgc tatctcagcc tggcgcaaaa cgacatccac agccgtgtgt	1860
cccagcagct ctgcagcgc tcgctgcggg ccttggaactt cagcggcaat gccttgagcc	1920
ggatgtgggc cgaggagac ctgtatctcc acttcttccg aggcctgagg agcctggtcc	1980
ggttggaact gtcccagaat cgctgcata cctcttgcc acgcacctg gacaacctcc	2040
ccaagagcct gcggtgctg cgtctccgtg acaattatct ggctttcttc aactggagca	2100
gcctggctct cctccccagg ctggaagccc tggacctggc gggaaaccag ctgaaggccc	2160
tgagcaacgg cagcttgctt aatggaacct agctccagag gctggacctc agcagcaaca	2220
gtatcagctt cgtggcctcc agcttttttg ctctggccac caggctgcga gagctcaacc	2280
tcagtgccaa cgccctcaag acggtggagc cctcctgggt cggttctcta gcgggcaccc	2340
tgaaagtctt agatgtgact ggcaaccccc tgcactgcgc ctgtggggcg gccttcgtgg	2400
acttcttgct ggaggtgcag gctgcagtgc ccggcctgcc aggccacgtc aagtgtggca	2460
gtccaggtea gctccagggc cgcagcatct ttgcgagga tctgcgcctc tgccctggatg	2520
aggccctctc ctgggactgt tttggcctct cgctgctgac cgtggccctg ggcctggccg	2580

tgcccatgct gcaccacctc tgtggctggg acctctggta ctgcttcac ctgtgcctgg 2640  
 cctggctgcc ccggcggggg cggcggcggg gcgcggatgc cctgccctac gatgcctttg 2700  
 tggctcttga caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760  
 ggctagagga gcgccgtgga cgcgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820  
 tacccggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880  
 tgtttgtgct ggcccacaca gacaggggtca gggcctctt gcgcgccagc tttctgctgg 2940  
 ccagcagcgc cctgctggag gaccgcaagg acgttggtgt gctgggtgatc ctgcgccccg 3000  
 acgcccaccg ctcccgtat gtgcggctgc gccagcgcct ctgccgccag agcgtcctcc 3060  
 tctggcccga ccagcccagt ggccagcga gcttctgggc ccagctgggc acggccctga 3120  
 ccagggacaa ccagcacttc tataaccaga acttctgccg gggcccccacg acggcagagt 3180  
 gaccgcccag caccacaagc ctccctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28

<211> 2460

<212> DNA

<213> *Felis catus*

<400> 28

atggggccct gccatggcgc cctgcacccc ctgtctctcc tgggtgcaggc tgccgcgctg 60  
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgcac 120  
 ggctgggtga attgcgactg gctgttcctc aagtccgtgc ccacttctc ggccgcagcg 180  
 ccccgctggtg acgtcaccag cctttccctg tactccaacc gcaccacca cctccacgac 240  
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaatggaa ctgcccaccc 300  
 gccagcctca gcccctgca ctccctctgt cacatgacca ttgagcccca caccttctgt 360  
 gccgtgcccga ccctggagga gctgaacctg agctacaaca gcatcacgac agtaccgcgc 420  
 ctgcccagtt ccctcgtgtc cctgtccttg agccgtacca acatcctggg gctggacct 480  
 gccaacctcg cagggtctga ctccctgcgc tttctgttcc tggatggcaa ctgctactac 540  
 aagaaccctt gccgcaggc cctgcagggt gccccgggcg ccctccttgg cctgggcaac 600  
 cttacgcacc tgtcactcaa gtacaacaac ctcaactgcg tgccccgcgg cctgcccccc 660  
 agcctggagt acctgctatt gtctacaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaacctga ccgcctcgc tgtgtctgat gtgggtggga actgccgtcg ctgtgaccac 780  
 gcccgcaacc cctgtatgga gtgcccgaag ggcttcccg cactgcaccc tgacaccttc 840  
 agccacctga accacctga aggcctgggt ttgaaggaca gctctctcta caacctgaac 900



cccagatggg tccatgccct gggcaacctc atgggtgctgg acctgagtga gaacttccta 960  
 tatgactgca tcacaaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac 1020  
 ttgtctttca attaccacaa gaaggtgtcc ttgtcccacc tgcactctggc gccctccttc 1080  
 gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttcog ctcgctcagc 1140  
 gagaccacgc tccggtcgct ggtccacctg cccatgctcc agagtctgca cctgcagatg 1200  
 aacttcatca atcaggccca gctcagcctc ttcggggcct tccctggcct gcgatacgtg 1260  
 gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg 1320  
 gatggtgggg agagagtccg gctgccatct ggggacctag ctctggggcc accgggcacc 1380  
 cctagctccg agggcttcat gccaggctgc aagacctca acttcacctt ggacctgtca 1440  
 cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc 1500  
 ctgctcctga gccgcaacag catctcgagc gcagtcaacg gtcacaatt tatgccgtg 1560  
 accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct 1620  
 ttcacggagc tgccgcggct ggaggccctg gacctcagct acaacagcca gcccttcagc 1680  
 atgcaggggc tgggtcacia cctcagcttt gtggcacagc tgccggccct gcgctatctc 1740  
 agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgctg 1800  
 cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat 1860  
 ctccacttct tccgaggcct gaggagcctg gtccggttgg atctgtccca gaatcgctg 1920  
 cataccctct tgccacgcac cctggacaac ctcccaga gcctgcggct gctgcgtctc 1980  
 cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa 2040  
 gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaattga 2100  
 acccagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt 2160  
 tttgctctgg ccaccaggtc gcgagagctc aacctcagt ccaacgccct caagacgggtg 2220  
 gagccctcct ggttcgggtc tctagcgggc accctgaaag tcctagatgt gactggcaac 2280  
 cccctgcact gcgcctgtgg gggggccttc gtggacttct tgctggaggt gcaggtgca 2340  
 gtgcccggcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc 2400  
 atctttgcgc aggatctgcg cctctgcctg gatgaggccc tctcctggga ctgttttggc 2460

<210> 29

<211> 1032

<212> PRT

<213> Mus musculus

&lt;400&gt; 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225		230		235		240
Ala Asn Leu Thr Ser	Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg					
	245		250		255	
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser						
	260		265		270	
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly						
	275		280		285	
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe						
	290		295		300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu						
305		310		315		320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu						
	325		330		335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala						
	340		345		350	
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu						
	355		360		365	
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu						
	370		375		380	
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met						
385		390		395		400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala						
	405		410		415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr						
	420		425		430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu						
	435		440		445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser						
	450		455		460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp  
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser  
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val  
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe  
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser  
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 30  
 <211> 821  
 <212> PRT  
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser  
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe  
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340	345	350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
355	360	365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
370	375	380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
405	410	415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
420	425	430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
435	440	445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
450	455	460
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu		
465	470	475
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu		
485	490	495
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala		
500	505	510
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp		
515	520	525
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu		
530	535	540
Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe		
545	550	555
Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser		
565	570	575



Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly  
820

<210> 31

<211> 3200

<212> DNA

<213> Mus musculus

<400> 31

tgtcagaggg agcctcggga gaatcctcca tctcccaaca tggttctccg tgaaggact	60
ctgcaccctt tgtccctcct ggtacagggt gcagtgtctg ctgagactct ggccctgggt	120
accctgcctg ccttcctacc ctgtgagctg aagcctcatg gcctgggtga ctgcaattgg	180
ctgttcttga agtctgtacc ccgtttctct gcggcagcat cctgctcaa catcaccgc	240
ctctccttga tctccaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc	300
aacctgcggc agctgaacct caagtggaa tgtccacca ctggccttag cccctgcac	360
ttctcttgcc acatgaccat tgagcccaga accttcttgg ctatgcgtac actggaggag	420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctggtgaat	480
ctgagcctga gccacaccaa catcctgggt ctagatgcta acagcctcgc cggcctatac	540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg	600
gtgaagggtga cccagggcgc cctcctgggc ctgagcaatc tcaccatct gtctctgaag	660
tataacaacc tcacaaaggt gcccgcgcaa ctgccccca gcctggagta cctcctggtg	720
tcctataacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttga	780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgaccatg ccccaatcc ctgtatagaa	840
tgtggccaaa agtccctcca cctgcacct gagaccttcc atcacctgag ccatctggaa	900
ggcctggtgc tgaaggacag ctctctccat aactgaact cttcctgggt ccaaggctctg	960
gtcaacctct cgggtgctga cctaagcgag aactttctct atgaaagcat caaccacacc	1020
aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag	1080
aaggatctct ttgcccgcct ccacctggca agttccttca agaacctgggt gtactgcag	1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg	1200
gccgatctgc caaaactcca cactctgcat cttcaaatga acttcatcaa ccaggcacag	1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcatc	1320
agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag	1380
gagctgttgt ctgcggatcc tcaccagct cactgagca cccctgcttc taagaacttc	1440

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgcctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttcttgccgc tgactaatct gcaggtgctg	1620
gacctgtccc ataacaaact ggacttgtag cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc	1860
ggcaacggta tgggcccgc atgtgggatgag gggggccttt atctccattt cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcatacct cccgccccag	1980
aaccttgaca acctcccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttcctg cccaacctgg aagtccatga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaata gcaacctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct gccggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
cccattgtga tgaacctgac agttcttagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttgag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcact cttggctgtg	2520
gccgtgggca tgggtgtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccgc gccgacgcag cgcaccaagct	2640
ctccccatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacgg accgcgtcag tggcctcctg	2880
cgcaccagct tcctgtggc tcagcagcgc ctgttggaag accgcaagga cgtggtggtg	2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgtatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggcc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgccgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcatctt catgcctggt	3180
tcccagttg ctctgcctgc	3200

<210> 32  
 <211> 2463  
 <212> DNA  
 <213> Mus musculus

<400> 32  
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagaggc tgcagtgtcg 60  
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120  
 ggctgggtgg actgcaattg gctgttcctg aagtctgtac cccgtttctc tgcggcagca 180  
 tcctgctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240  
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300  
 actggcctta gccccctgca cttctcttgc cacatgacca ttgagcccag aaccttctcg 360  
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420  
 ctgcccagct ccctgggtgaa tctgagcctg agccacacca acatcctggg tctagatgct 480  
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctc gcacaggagc ggtgaagggtg accccaggcg cctcctggg cctgagcaat 600  
 ctcacccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctggg gtccctataac ctcatgtgca agctggggcc tgaagacctg 720  
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780  
 gcccccaatc cctgtataga atgtggccaa aagtcctcc acctgcacc tgagaccttc 840  
 catcacctga gccatctgga aggccctggg ctgaaggaca gctctctcca tacactgaac 900  
 tcttcctggg tccaaggctc ggtcaacctc tcggtgctgg acctaaagcg gaactttctc 960  
 tatgaaagca tcaaccacac caatgccttt cagaacctaa cccgcctgcg caagctcaac 1020  
 ctgtccttca attaccgcaa gaaggatatc ttgcccgc tccacctggc aagttccttc 1080  
 aagaacctgg tgctactgca ggagctgaac atgaacggca tcttcttccg ctcgctcaac 1140  
 aagtacacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaatg 1200  
 aacttcatca accaggcaca gctcagcatc ttgtgtacct tccgagccct tcgctttgtg 1260  
 gacttgtcag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320  
 gcagatgatg cagagcagga ggagctgttg tctgcggatc ctcaccagc tccactgagc 1380  
 accctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440  
 tctcggaaca acctgggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500  
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgccg 1560

```

ctgactaatc tgcagggtgct ggacctgtcc cataacaaac tggacttgta ccactggaaa 1620
tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680
agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740
cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800
gtgagggttc ttgacttcag cggcaacggt atgggccgca tgtgggatga ggggggcctt 1860
tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920
ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980
ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttcct gcccaacctg 2040
gaagtcctag acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaata 2100
ggcaccctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160
ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220
gtggatcgct cctggttttg gccattgtg atgaacctga cagttctaga cgtgagaagc 2280
aaccctctgc actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340
aagggtgcctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400
agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460
ggc 2463

```

```

<210> 33
<211> 1032
<212> PRT
<213> Homo sapiens

```

```

<400> 33

```

```

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
          20           25           30

```

```

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
          35           40           45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
          50           55           60

```

```

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
                   85                                  90                                  95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
                   100                                  105                                  110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
                   115                                  120                                  125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
                   130                                  135                                  140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
                   145                                  150                                  155                                  160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
                   165                                  170                                  175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
                   180                                  185                                  190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
                   195                                  200                                  205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
                   210                                  215                                  220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
                   225                                  230                                  235                                  240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
                   245                                  250                                  255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
                   260                                  265                                  270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
                   275                                  280                                  285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
                   290                                  295                                  300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

- 96 -

- 97 -



Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val  
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp  
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu  
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg  
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu  
1025 1030

<210> 34  
<211> 820  
<212> PRT  
<213> Homo sapiens  
  
<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala  
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu  
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420	425	430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu		
435	440	445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu		
450	455	460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser		
465	470	475
480		
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser		
485	490	495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val		
500	505	510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu		
515	520	525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu		
530	535	540
Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly		
545	550	555
560		
Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr		
565	570	575
Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser		
580	585	590
Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn		
595	600	605
Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe		
610	615	620
Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635
640		
His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln		
645	650	655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala  
820

<210> 35

<211> 3352

<212> DNA

<213> Homo sapiens

<400> 35

aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60

ggacctcgag tgtgaagcat ccttcctgt agctgctgtc cagtctgccc gccagacct 120

ctggagaagc ccctgcccc cagcatgggt ttctgccgca gcgcctgca cccgctgtct 180

ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gctgccttc 240

ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcacccccgt ggcaatgtca ccagcctttc cttgtcctcc	360
aaccgcatcc accacctcca tgattctgac tttgcccacc tgcccagcct gcggcatctc	420
aacctcaagt ggaactgccc gccggttggc ctcagcccca tgcacttccc ctgccacatg	480
accatcgagc ccagcacctt cttggctgtg ccacacctgg aagagctaaa cctgagctac	540
aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat	600
accaacatcc tgatgctaga ctctgccagc ctcgccggcc tgcattgccct gcgcttccta	660
ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggcaactgga ggtggccccg	720
ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact	780
gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgtccta caaccgcatc	840
gtcaaaactgg cgcctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc	900
ggaaattgcc gccgctgcca ccacgctccc aaccctgca tggagtgcgc tcgtcacttc	960
ccccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag	1020
gacagttctc tctcctggct gaatgccagt tggttccgtg ggctgggaaa cctccgagtg	1080
ctggacctga gtgagaactt cctctacaaa tgcatacta aaaccaaggc cttccagggc	1140
ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggt gtcctttgcc	1200
cacctgtctc tggccccctc cttcgggagc ctggctgccc tgaaggagct ggacatgcac	1260
ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccc cctgccccatg	1320
ctccagactc tgcgtctgca gatgaacttc atcaaccagg ccagctcgg catcttcagg	1380
gccttccctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag	1440
ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac	1500
cttgcctcgg cccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc	1560
ctcaacttca ccttgatct gtacgggaac aacctggtga ccgtgcagcc ggagatgttt	1620
gccagctct cgcacctgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc	1680
aatggctccc agttcctgcc gctgaccggt ctgcagggtc tagacctgtc ccgcaataag	1740
ctggacctct accacgagca ctcatcacg gagctaccgc gactggaggc cctggacctc	1800
agctacaaca gccagccctt tggcatgcag ggcgtgggcc acaacttcag cttcgtggct	1860
cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc	1920
cagcagctct gcagtacgtc gctgcccccc ctggacttca gcggcaatgc actgggccat	1980
atgtggggcc aggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg	2040

ctggacttgt cccagaaccg cctgcacacc ctctgcccc aaaccctgcg caacctcccc 2100  
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc 2160  
 ctccacttcc tgcccaaact ggaagtcctc gacctggcag gaaaccggct gaaggccctg 2220  
 accaatggca gcctgcctgc tggcaccggt ctccggaggc tggatgtcag ctgcaacagc 2280  
 atcagcttcg tggcccccg cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340  
 agcgccaacg ccctcaagac agtggaccac tcttggtttg ggccctggc gagtgcctg 2400  
 caaatactag atgtaagcgc caacctctg cactgcgcct gtggggcggc ctttatggac 2460  
 ttctgctggt aggtgcaggc tgccgtgccc ggtctgcca gccgggtgaa gtgtggcagt 2520  
 ccgggccagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag 2580  
 gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg 2640  
 cccatgctgc atcacctctg tggctgggac ctctggtact gcttcacct gtgcctggcc 2700  
 tggcttcctt ggcgggggcg gcaaagtggg cgagatgagg atgccctgcc ctacgatgcc 2760  
 ttctggtctc tcgacaaaac gcagagcgca gtggcagact ggggtgtaca cgagcttcgg 2820  
 gggcagctgg aggagtgcog tgggcgctgg gcaactccgc tgtgcctgga ggaacgcgac 2880  
 tggctgcctg gaaaaaccct ctttgagaac ctgtgggcct cggctctatg cagccgcaag 2940  
 acgtgtttg tgctggcca caccgaccgg gtcagtggtc tcttgcgcg cagcttctg 3000  
 ctggcccagc agcgctgct ggaggaccgc aaggacgtcg tggtgctggt gatcctgagc 3060  
 cctgacggcc gccgctcccg ctacgtgcgg ctgcgccagc gcctctgcc ccagagtgtc 3120  
 ctctctggc cccaccagcc cagtggctcag cgcagcttct gggcccagct gggcatggcc 3180  
 ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa 3240  
 tagccgtgag ccggaatcct gcacgggtgcc acctccacac tcacctcacc tctgcctgcc 3300  
 tggctgacc ctccctgct cgctccctc accccacacc tgacacagag ca 3352

&lt;210&gt; 36

&lt;211&gt; 2460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

atgggtttct gccgcagcgc cctgcaccg ctgtctctcc tggcgcaggc catcatgctg 60  
 gccatgaccc tggccctggg taccttgcc gccttctac cctgtgagct ccagccccac 120  
 ggctggtga actgcaactg gctgttctc aagtctgtgc ccaacttctc catggcagca 180  
 ccccggtgca atgtcaccag ctttctctg tctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgcg	300
gttggcctca gcccacatgca cttccctcgc cacatgacca tcgagcccag caccttcttg	360
gctgtgcca ccttggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg	420
ctgccc aaat cctcataatc cctgtccctc agccatacca acatcctgat gctagactct	480
gccagcctcg cgggcctgca tgccctgcgc ttccatttca tggacggcaa ctgttattac	540
aagaaccctt gcaggcaggc actggagggtg gcccgggtg ccctccttgg cctgggcaac	600
ctcaccaccc tgtcactcaa gtacaacaac ctcaactgtg tgccccgcaa cctgccttcc	660
agcctggagt atctgctgtt gtccataaac cgcacgtcga aactggcgcc tgaggacctg	720
gccaatctga ccgccctgcg tgtgctcgat gtgggaggaa attgccgcg ctgcgaccac	780
gctcccaacc cctgcatgga gtgccctcgt cacttcccc agctacatcc cgataccttc	840
agccacctga gccgtcttga aggcctgggtg ttgaaggaca gttctctctc ctggctgaat	900
gccagttggt tccgtgggct gggaaacctc cgagtgtgtg acctgagtga gaacttcctc	960
tacaaatgca tcaactaaac caaggccttc cagggcctaa cacagctgcg caagcttaac	1020
ctgtccttca attacaaaa gaggtgtcc ttgcccacc tgtctctggc cccttccttc	1080
gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttccg ctcaactgat	1140
gagaccacgc tccggccact ggccgcctg cccatgtccc agactctgcg tctgcagatg	1200
aacttcatca accaggccca gctcggcac ttccaggcct tccctggcct gcgctacgtg	1260
gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca	1320
gatggagggg agaaggctctg gctgcagcct ggggaccttg ctccggcccc agtggacact	1380
cccagctctg aagacttcag gcccactgc agcaccctca acttcacctt ggatctgtca	1440
cggacaaccc tggtgaccgt gcagccggag atgtttgccc agctctcgca cctgcagtgc	1500
ctgcgcctga gccacaactg catctcgagc gcagtcaatg gctcccagtt cctgccgctg	1560
accggtctgc aggtgctaga cctgtcccg c aataagctgg acctctacca cgagcactca	1620
ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc	1680
atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgcaccct gcgccacctc	1740
agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgctg	1800
cgggccctgg acttcagcgg caatgcactg ggccatatgt gggccgaggg agacctctat	1860
ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgtccca gaaccgctg	1920
cacaccctcc tgcccaaac cctgcgcaac ctcccaaga gcctacaggt gctgcgtctc	1980
cgtgacaatt acctggcctt ctttaagtgg tggagcctcc acttctgcc caaactggaa	2040



gtcctcgacc tggcaggaaa ccggctgaag gccctgacca atggcagcct gcctgctggc 2100  
 acccggtccc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc ccccggttc 2160  
 tttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220  
 gaccactcct ggtttgggcc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280  
 cctctgcact gcgcctgtgg ggccggccttt atggacttcc tgctggaggt gcaggetgcc 2340  
 gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccgg gccagctcca gggcctcagc 2400  
 atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37  
 <211> 26  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 37  
 accttgccctg ccttcctacc ctgtga 26

<210> 38  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 38  
 gtccgtgtgg gccagcaca a 21

<210> 39  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 39  
 tccatgacgt ttttgatgtt 20

<210> 40  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 40  
tccataacgt ttttgatggt 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 41  
tccatcacgt ttttgatggt 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 42  
tccattacgt ttttgatggt 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 43  
tccatggcgt ttttgatggt 20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 44  
tccatgccgt ttttgatggt 20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgctcgt ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 50  
tccatgacct ttttgatggt 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 51  
tccatgactt ttttgatggt 20

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 52  
tccatgacgc ttttgatggt 20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 53  
tccatgacga ttttgatggt 20

<210> 54  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 54  
tccatgacgg ttttgatggt 20

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 55  
tccatgacgt ctttgatggt 20

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 56  
tccatgacgt atttgatggt 20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 57  
tccatgacgt gtttgatggt 20

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 58  
tcgtcgtttt gtcgttttgt cggt 24

<210> 59  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 59  
tgctgctttt gtgcttttgt gctt 24

<210> 60  
<211> 20  
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys  
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys  
 1 5 10 15

<210> 64  
 <211> 16  
 <212> PRT  
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys  
 1 5 10 15

<210> 65  
 <211> 31  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Consensus oligopeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                  25                  30

<210> 66  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
   1                  5                  10                  15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                  25                  30

<210> 67  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid



<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 68  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His  
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr  
 20 25 30

<210> 69  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

```
<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 70
tccaggactt ctctcaggtt
```